


```

; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO: 1286
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1286

Query Match          11.6%; Score 69; DB 6; Length 653;
Best Local Similarity 33.8%; Pred. No. 5.1;
Matches 26; Conservative 12; Mismatches 31; Indels 8; Gaps 4;

QY 10 ELKRIAS---MAGROKRPAREILTRSELDQY-YELSEK-RKNEPLAGFAA--KEAFSK 61
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 536 EIERMVNDAEKFAEDDKLKERIDTRNELESYAYSLKQIGDKELGKLSSEDKETMEK 595
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 62 AFGTIGRQLSFQDIEI 78
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 596 AVEKEIEMLESHQDADI 612
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 3
US-10-467-657-694
; Sequence 694, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO: 694
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-694

Query Match          11.0%; Score 65.5; DB 6; Length 558;
Best Local Similarity 26.6%; Pred. No. 10;
Matches 34; Conservative 29; Mismatches 36; Indels 29; Gaps 9;

QY 5 GIDITELKRIASMAGRO--KRPAREILTRSELDQY--LSEKR-----KNEF--LAGRF 53
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 76 GLAV-ENERLATQIGERKFAFAEYALERQINQRYETDLEERQYVRDVQNDLSVGKRF 134
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 54 AAKEAFSKAFGTIGRQLSF-ODIEIRKQNGKPYITCTKLSQAAVHVSITTKRYAAQ 112
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 135 AAEE-----KQIAYILOKEAEERLRQSH---TELQEKQAQGLAVEN--ERLATQ 178
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 113 VIERLSS 120
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 179 IEQERLAS 186
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 4
US-10-467-657-3066
; Sequence 3066, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
```

```

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO: 3066
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3066

Query Match          10.7%; Score 63.5; DB 6; Length 141;
Best Local Similarity 27.6%; Pred. No. 2.9;
Matches 32; Conservative 22; Mismatches 31; Indels 31; Gaps 8;

QY 18 AGROKRPAREILT-RSELDQYELSEKRN--EPLAGFAKFAF---SKA----- 62
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 15 AAQTWADTVFSCKTDNNKXIEYQKINRLYEYSPSAKKEIAIRNSRADLLGRSDRW 74
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 63 FGTIGRQLSFQDIEIRKQNGK-PYIICTKLSQAAVHVSITTKRYAAQVIER 117
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 75 QGMSGRRAIV-----KFQNGEFMTWTGTFD-----SVTITE---SSGVVER 115
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 5
US-10-793-626-3184
; Sequence 3184, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3184
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3184

Query Match          10.6%; Score 63; DB 6; Length 567;
Best Local Similarity 29.9%; Pred. No. 19;
Matches 26; Conservative 15; Mismatches 36; Indels 10; Gaps 4;

QY 2 YGIDITELKRIASMAGROKRPAREILTRSELDQYEL-----SEKRNELAGRFPAKE 57
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 380 YGDRFRITQIGMLDGSQ-VAQFAEGI---EVQGVRLGTKYSSEMNATFLDNQKRAQ 434
   |||:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
QY 58 AFSKAFGTIGRQLSFQDIEIRKQNG 84
   |||:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
DB 435 LIMCYGIGVSRILS-AIVEQNNDENG 460
   |||:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|

RESULT 6
US-10-927-641-77
; Sequence 77, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Ranjan
; APPLICANT: Rice, Stephen
```

```

; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-927-641-77
```

```

Query Match          10.6%; Score 63; DB 6; Length 805;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 24; Conservative 17; Mismatches 27; Indels 22; Gaps 4;

QY 2 YGIGDITLKRILASAGQKRPFAERILRLSELDQYELSEKRNFLAGFAKAFK 61
DB 592 YGNSKRLRLANLVVGGSRKDSKDLSESEKKNYDLEKX--LNGQF----- 640
QY 62 AFGTGIGRLSPQDIEIRKDKNGKPY-IIC 90
DB 641 -----RWISSQMRVR---NGELYRYIC 660
```

```

RESULT 7
US-11-194-246-286
; Sequence 286, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidsson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (MAR 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 286
; LENGTH: 308
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-286
```

```

Query Match          10.5%; Score 62.5; DB 7; Length 308;
Best Local Similarity 27.1%; Pred. No. 9.9;
Matches 19; Conservative 10; Mismatches 18; Indels 23; Gaps 2;
```

```

QY 38 YELSEKRNFLAGFAKAFKAFK-----TGIGRLSPQDIEIR 79
DB 126 FKFGSKRQ-----GNFAMLOASKRFGFIVEDNRSFCIDQAQRISTAIRLANDDQLA 180
QY 80 KDQNGKPYII 89
DB 181 ENLIGKPYRI 190
```

```

RESULT 8
US-10-793-626-1318
; Sequence 1318, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1318
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1318
```

```

Query Match          10.5%; Score 62.5; DB 6; Length 525;
Best Local Similarity 26.8%; Pred. No. 19;
Matches 26; Conservative 13; Mismatches 31; Indels 27; Gaps 4;

QY 19 GROKFAERILTRSLDQYELSEKRN-----KNEFLAGFAKAFKAFGTGIGR 69
DB 49 GRIYISEKI--GPELRQYFANDNEGKPFPSRDYKIVLAKYKSR---WISFQTG--- 100
QY 70 QLSFQDIEIRKDKNGKPYIICTKLSQAAVHSITHTK 106
DB 101 -----KDYEGFYIQTMTMPPLQATDELHIDHTE 127
```

```

RESULT 9
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
```

NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 2725
TYPE: PRT
ORGANISM: Homo sapiens
US-11-113-424-52

Query Match 10.4%; Score 62; DB 7; Length 2725;
Best Local Similarity 27.4%; Pred. No. 1.7e+02;
Matches 29; Conservative 15; Mismatches 50; Indels 12; Gaps 4;

QY 12 KRISAGRO-KRPFERITRSELDQYVELSEKRNFLAGFAKFAFGTGIQRQ 70
DB 2016 ROTGLIRGQIFRESEGLVNAKRPDYSY-----NMF---RYTSMQAVINETPLPID-L 2064
QY 71 LSPDIEIRKQNGKPYIITKLSQAAMVSVITHTKEXAAQVIE 116
DB 2065 YRYVDVSGRTEQFGKFSVINYDINQVITTTVMKHTKIFSANGQVIE 2110

RESULT 10
US-10-467-657-2290
Sequence 2290, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 2290
LENGTH: 228
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2290

Query Match 10.3%; Score 61.5; DB 6; Length 228;
Best Local Similarity 26.7%; Pred. No. 8.7;
Matches 28; Conservative 8; Mismatches 32; Indels 37; Gaps 5;

QY 8 ITELKRIS-MAGROKRFARILITRSELDQYVELSEKRNFLAGFAKFAFG-- 64
DB 25 LPEARTRAGRLIGRLORFVGSV--KQELDTQIELEBK-----VKQAFEAQAQV 73
QY 65 -----TGIGRQLSPDI-----EIRKQNGKP 86
DB 74 RDLAKETDTMQNSLHDISDGLKPEWKEPEQRTPADFGVDENGPN 118

RESULT 11
US-11-179-977-19
Sequence 19, Application US/11179977
Publication No. US20050249789A1
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
FILE REFERENCE: GC511-PCT
CURRENT APPLICATION NUMBER: US/11/179,977
CURRENT FILING DATE: 2005-07-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 240
TYPE: PRT

ORGANISM: Bacillus
US-11-179-977-19

Query Match 10.3%; Score 61.5; DB 7; Length 240;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 37; Conservative 14; Mismatches 45; Indels 49; Gaps 7;

QY 5 GLDITELKRISAMGROKRFARILITRSELDQ-----YVELSEKRNFLAG----- 51
DB 46 GHDFRIGRI---GRQ---VEELSKREIDRIIGVPIKDYERANTYHPESKFSAY 98
QY 52 -RFAKFAFSKA-----FGTIGROU-----SPDIEIRKQNGK 85
DB 99 KRFAIHELVPADDEVPYLGVCRTLIGSLGATVELMTALDYPNFMGNIMQSPYVDK 158
QY 86 PYITCKLSQAAMVSVITHTKEXAAQVIE 107
DB 159 HVLAVKQSDIDIKLSIYHQTGKE 183

RESULT 12
US-10-793-626-1900
Sequence 1900, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1900
LENGTH: 300
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-1900

Query Match 10.3%; Score 61.5; DB 6; Length 300;
Best Local Similarity 20.7%; Pred. No. 12;
Matches 29; Conservative 26; Mismatches 46; Indels 39; Gaps 5;

QY 4 IGLDITELKRISAMGROK---RFAIRILTR-----SELDQYVE 39
DB 76 VGTVAVLTSVAMIPGHEAVFVNFPSRLITLALIGLVAGLVNFIILPPKYYHOLEQOLA 135
QY 40 LSEK-----RQNEFLAGFAKFAFSKAFGTGIQRQ-----LSFDIEIRKQNGKP 86
DB 136 LSEKMYRLFYERCNELLGKFSSEKTSKELSKINTIAQKVTLMSTQRODELHYHKNEDN 195
QY 87 YIICTKLSQAAMV--VSITH 104
DB 196 WKLANRLTRAYNNRLPFI 215

RESULT 13
US-11-055-822-316
Sequence 316, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krieger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zeidler, Oskar
APPLICANT: Habertauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN

```

CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 316
LENGTH: 217
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-316

```

```

Query Match      10.1%; Score 60; DB 7; Length 217;
Best Local Similarity 31.2%; Pred. No. 12;
Matches 30; Conservative 12; Mismatches 28; Indels 26; Gaps 6;

```

```

QY 34 LDQYVLS--EK-----RKNEFLAGFAKFAFSKFGGICRQSLFQDIETKXQ 82
DB 24 LHFHQLHLEKLVVHSDIRAEFGDARWCAHQHL--QLGRDSD-----PILRGE 75
QY 83 NGKPYIICTLSQAAYVHSITHTKEYAAQVIERL 118
DB 76 RGMP-----LWPSVSGSLTHDGFRAA--VVAPEL 104

```

```

RESULT 14
US-10-467-657-34
Sequence 34, Application US/10467657
Publication NO. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIIGNANI Vega
APPLICANT: MONACT Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 34
LENGTH: 327
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-34

```

```

Query Match      10.1%; Score 60; DB 6; Length 327;
Best Local Similarity 24.5%; Pred. No. 20;
Matches 36; Conservative 21; Mismatches 44; Indels 46; Gaps 7;

```

```

QY 12 KRISMAGROKRFERILITRSELDQYVLSKRN-----FLAGFAKFAKFAKFAKFAK 65

```

```

DB 17 KRAKESTRQERAVKAGTVANVDR--NRLSARSKAKENIARMLSG---AKVSEDEALTTC 72
QY 66 GIGRQLSFQDIETKXQ-----NGKPYII--CTKLSQAAY 98
DB 73 GIMMRLSLQDMRYACNQELINFAEHYKQVRLGLYCTDTPANGESVLPACREASQAV 132
QY 99 HVSITHTKEY-----AAQVIERLSS 120
DB 133 Q-----WTKDFNLSPNQRLVLRPLSN 155

```

```

RESULT 15
US-10-467-657-8374
Sequence 8374, Application US/10467657
Publication NO. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIIGNANI Vega
APPLICANT: MONACT Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 8374
LENGTH: 341
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8374

```

```

Query Match      10.1%; Score 60; DB 6; Length 341;
Best Local Similarity 24.5%; Pred. No. 21;
Matches 36; Conservative 21; Mismatches 44; Indels 46; Gaps 7;

```

```

QY 12 KRISMAGROKRFERILITRSELDQYVLSKRN-----FLAGFAKFAKFAKFAKFAK 65
DB 31 KRAKESTRQERAVKAGTVANVDR--NRLSARSKAKENIARMLSG---AKVSEDEALTTC 86
QY 66 GIGRQLSFQDIETKXQ-----NGKPYII--CTKLSQAAY 98
DB 87 GIMMRLSLQDMRYACNQELINFAEHYKQVRLGLYCTDTPANGESVLPACREASQAV 146
QY 99 HVSITHTKEY-----AAQVIERLSS 120
DB 147 Q-----WTKDFNLSPNQRLVLRPLSN 169

```

```

Search completed: December 21, 2005, 14:13:52
Job time : 9.35821 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 21, 2005, 13:49:45 ; Search time 133.134 Seconds
(without alignments)
376.608 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595

Sequence: 1 AVGIGDITELKRIASMAGR.....SITHTKEYAAQVIERLSS 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	100.0	120	US-09-770-834-2	Sequence 2, Appl
2	595	100.0	120	US-10-717-138-2	Sequence 2, Appl
3	591	99.3	121	US-09-771-383-1	Sequence 1, Appl
4	591	99.3	121	US-09-771-383-11	Sequence 11, Appl
5	591	99.3	121	US-09-770-834-12	Sequence 12, Appl
6	591	99.3	121	US-10-717-138-12	Sequence 12, Appl
7	304	51.1	119	US-10-282-122A-46229	Sequence 46229, A
8	287	48.2	118	US-10-282-122A-60496	Sequence 60496, A
9	281.5	47.3	124	US-10-724-972A-3855	Sequence 3855, Ap
10	279.5	46.8	117	US-10-282-122A-70857	Sequence 70857, A
11	278.5	46.8	119	US-10-282-122A-71569	Sequence 71569, A
12	278	46.7	119	US-09-771-383-5	Sequence 5, Appl
13	278	46.7	119	US-09-770-834-6	Sequence 6, Appl
14	278	46.7	119	US-10-717-138-6	Sequence 6, Appl
15	277	46.6	119	US-09-815-242-5341	Sequence 5341, Ap
16	277	46.6	119	US-09-815-242-12401	Sequence 12401, A
17	275	46.2	119	US-10-282-122A-44196	Sequence 44196, A
18	275	46.2	119	US-10-857-625-722	Sequence 722, App
19	269	45.2	117	US-10-282-122A-57376	Sequence 57376, A
20	269	45.2	117	US-10-953-901-230	Sequence 230, App
21	269	45.2	117	US-10-953-901-232	Sequence 232, App
22	267	44.9	117	US-09-815-242-10776	Sequence 10776, A
23	262	44.0	126	US-10-282-122A-52394	Sequence 52394, A
24	250	42.0	117	US-10-501-282-74	Sequence 74, Appl
25	244	41.0	113	US-10-282-72	Sequence 72, Appl
26	243	40.8	120	US-10-282-122A-74124	Sequence 74124, A
27	243	40.8	120	US-10-472-928-5504	Sequence 3504, Ap

28	243	40.8	122	3	US-09-815-242-13472	Sequence 13472, A
29	243	40.8	122	3	US-09-815-242-13649	Sequence 13649, A
30	243	40.8	122	3	US-09-897-645-1	Sequence 1, Appl
31	243	40.8	157	5	US-10-617-320-4199	Sequence 4199, Ap
32	237.5	39.9	126	4	US-10-282-122A-77481	Sequence 77481, A
33	228.5	38.4	119	3	US-09-769-736-30	Sequence 30, Appl
34	227	38.2	119	4	US-10-282-122A-72422	Sequence 72422, A
35	221.5	37.2	124	4	US-10-282-122A-51630	Sequence 51630, A
36	221	37.1	118	4	US-10-282-122A-74722	Sequence 74722, A
37	219.5	36.9	126	4	US-10-282-122A-53026	Sequence 53026, A
38	209.5	35.2	126	4	US-10-282-122A-69169	Sequence 69169, A
39	201.5	33.9	169	3	US-09-771-383-6	Sequence 6, Appl
40	201.5	33.9	169	3	US-09-770-834-7	Sequence 7, Appl
41	201.5	33.9	169	4	US-10-717-138-7	Sequence 7, Appl
42	201	33.8	126	3	US-09-771-383-8	Sequence 8, Appl
43	201	33.8	126	3	US-09-770-834-9	Sequence 9, Appl
44	201	33.8	126	4	US-10-717-138-9	Sequence 9, Appl
45	200.5	33.7	126	4	US-10-282-122A-78498	Sequence 78498, A

ALIGNMENTS

```

RESULT 1
US-09-770-834-2
; Sequence 2, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Parisis, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; US-09-770-834-2

Query Match      100.0%; Score 595; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AVGIGDITELKRIASMAGRKRPFRILITRSELDQYELSEKRNKFLAGFAAKEARS 60
        |||
DB      1 AVGIGDITELKRIASMAGRKRPFRILITRSELDQYELSEKRNKFLAGFAAKEARS 60
        |||
QY      61 KAFGTIGRQLSFODIEIRKDONKRPYIICTKLQAQAAHVSIITHTKEYAAQVIERLSS 120
        |||
DB      61 KAFGTIGRQLSFODIEIRKDONKRPYIICTKLQAQAAHVSIITHTKEYAAQVIERLSS 120
        |||

RESULT 2
US-10-717-138-2
; Sequence 2, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Parisis, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark

```

```

; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/10/717,138
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-717-138-2
```

```

Query Match          100.0%; Score 595; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 AYGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 60
    |||||||
DB 1 AYGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 60
    |||||||
QY 61 KAFGTGIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 120
    |||||||
DB 61 KAFGTGIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 120
    |||||||
```

```

RESULT 3
US-09-771-383-1
; Sequence 1, Application US/09771383
; Patent No. US20020094562A1
; GENERAL INFORMATION:
; APPLICANT: Parriss, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
; TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
; FILE REFERENCE: 2368/12
; CURRENT APPLICATION NUMBER: US/09/771,383
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,639
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: B. subtilis
US-09-771-383-1
```

```

Query Match          99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 YGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 61
    |||||||
DB 3 YGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 62
    |||||||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 120
    |||||||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 121
    |||||||
```

```

RESULT 4
US-09-771-383-11
; Sequence 11, Application US/09771383
```

```

; Patent No. US20020094562A1
; GENERAL INFORMATION:
; APPLICANT: Parriss, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
; TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
; FILE REFERENCE: 2368/12
; CURRENT APPLICATION NUMBER: US/09/771,383
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,639
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Bacillus
US-09-771-383-11
```

```

Query Match          99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 YGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 61
    |||||||
DB 3 YGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 62
    |||||||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 120
    |||||||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 121
    |||||||
```

```

RESULT 5
US-09-770-834-12
; Sequence 12, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Parriss, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-770-834-12
```

```

Query Match          99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 YGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 61
    |||||||
DB 3 YGIGDITELKRIASMAGRQKRFARILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFSK 62
    |||||||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 120
    |||||||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTLSQAAPHVSIHTHKEYAAQVIERLSS 121
    |||||||
```

RESULT 6

US-10-717-138-12
Sequence 12, Application US/10717138
Publication No. US20040078147A1
GENERAL INFORMATION:
APPLICANT: Parriss, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/10/717,138
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/09/770,834
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
ORGANISM: Bacillus sp.
US-10-717-138-12

Query Match 99.3%; Score 591; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMAHQKRPARIILTRSLDQYELSEKKNIEFLAGRAAEAFSK 61
DB 3 YGIGDITELKRIASMAHQKRPARIILTRSLDQYELSEKKNIEFLAGRAAEAFSK 62
QY 62 AGGTGIGRQLSFQDIIEIRKQNGKPYIICTKLSQAAVHSITHTREYAAQVIERLSS 120
DB 63 AGGTGIGRQLSFQDIIEIRKQNGKPYIICTKLSQAAVHSITHTREYAAQVIERLSS 121

RESULT 7

US-10-282-122A-46229
Sequence 46229, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46229
LENGTH: 119
TYPE: PRT
ORGANISM: Bacillus anthracis
US-10-282-122A-46229

Query Match 51.1%; Score 304; DB 4; Length 119;
Best Local Similarity 54.2%; Pred. No. 2.3e-28;
Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

QY 3 GIGDITELKRIASMAHQKRPARIILTRSLDQYELSEKKNIEFLAGRAAEAFSK 62
DB 4 GIGDITELKRIASMAHQKRPARIILTRSLDQYELSEKKNIEFLAGRAAEAFSK 63
QY 63 FGTTGIGRQLSFQDIIEIRKQNGKPYIICTKLSQAAVHSITHTREYAAQVIERLSS 120
DB 64 VGTGIGRQLSFQDIIEIRKQNGKPYIICTKLSQAAVHSITHTREYAAQVIERLSS 119

RESULT 8

US-10-282-122A-60496
Sequence 60496, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

```

; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EILTRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 70857
LENGTH: 117
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70857

Query Match      47.0%; Score 279.5; DB 4; Length 117;
Best Local Similarity 51.3%; Pred. No. 2e-25;
Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4

Cy      2 YGIGDITELKRIISMAGROKPAERILT--RSELDQYELSEKRKNFPLAGRPAKEA 58
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      3 YGIGIDLEIRIKNLQ-NQTKFERILITIERDKLNY--THEQRRLFLAGRVTVEA 59
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||

Cy      59 FSKAFGTIGRGQLSFODIEIRKDNGKPYIICTKLSQLAAVHSITHTREVAAYQVIER 117
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      60 FSKALGTGLGSVSFOFDINCYNDAIGKP---CIDVPFYTHVSTHTENVAMSGVILER 115
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 11
US-10-282-122A-71569
Sequence 71569, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EILTRA.034A
```

Query Match	46.7%	Score 278;	DB 3;	Length 119;
Best Local Similarity	48.7%	Pred No. 3.1e-25;		
Matches 57;	Conservative 25;	Mismatches 31;	Indels 4;	Gaps 2

```

/ APPLICANT: Parris, Kevin
/ APPLICANT: Somers, William
/ APPLICANT: Tam, Amy
/ APPLICANT: Lin, Laura
/ APPLICANT: Stahl, Mark
/ APPLICANT: Powers, Robert
/ APPLICANT: Xu, Guan-Yi
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
/ TITLE OF INVENTION: OF B. SUBSTITIS ACP, AND USES THEREOF
/ FILE REFERENCE: 2368/14
/ CURRENT APPLICATION NUMBER: US/10/717,138
/ CURRENT FILING DATE: 2003-11-19
/ PRIOR APPLICATION NUMBER: US/09/770,834
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 60/202,466
/ PRIOR FILING DATE: 2000-05-08
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 6

```



```

1 CURRENT APPLICATION NUMBER: US/09/163,446
2 CURRENT FILING DATE: 1998-09-30
3 NUMBER OF SEQ ID NOS: 12
4 SOFTWARE: FASTSQ for Windows Version 3.0.
5 SEQ ID NO 4
6 LENGTH: 121
7 TYPE: PRT
8 ORGANISM: Streptococcus pneumonia
9 US-09-163-446-4

```

Query Match	99.3%	Score 591	DB 2	Length 121
Best Local Similarity	100.0%	Pred. No. 2.5e-63		
Matches 119	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 2 YGILDTTELKRIASMGQRKFAERILLTSELDQYVEISEKKNFPLGRFAAKAFSK 61

Db 3 YGILDTTELKRIASMGQRKFAERILLTSELDQYVEISEKKNFPLGRFAAKAFSK 62

QY 62 AFGTGISROLSPDIEIRKONGKPYIICTKLSQAAVHVSITHTKVEAAQAQVITEFLSS 120

63 AFGTGISROLSPDIEIRKONGKPYIICTKLSQAAVHVSITHTKVEAAQAQVITEFLSS 121

RESULT 3
US-09-770-834-12
; Sequence 12, Application US/09770834

```

: GENERAL INFORMATION:
: APPLICANT: Parris, Kevin
: APPLICANT: Somers, William
: APPLICANT: Tam, Amy
: APPLICANT: Lin, Laura
: APPLICANT: Stahl, Mark
: APPLICANT: Powers, Robert
: APPLICANT: Xu, Guan-Yi
: TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
: TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
: FILE REFERENCE: 2368/14
: CURRENT APPLICATION NUMBER: US/09/770, 834
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 60/202,466
: PRIOR FILING DATE: 2000-05-08
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 12
: LENGTH: 121
: TYPE: PRT
: ORGANISM: Bacillus sp.
: US-09-770-834-12

```

Query Match	99.3%;	Score 591;	DB 2;	Length 121;
Best Local Similarity	100.0%;	Pred. No. 2.5e-63;		
Matches 119;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2 YGIGDITIELKRIAMAGOKRFARILIRLSLDYELSEKKNIEFLAGRAAAEAVSK 61

Db 3 YGIGDITIELKRIAMAGOKRFARILIRLSLDYELSEKKNIEFLAGRAAAEAVSK 62

QY 62 AFGTGTGQOLSTODIEIRDDQNGKRYIICTKLSQAANVHSITHTTEYAAAOVIERLS 120

Db 63 AFGTGTGQOLSTODIEIRDDQNGKRYIICTKLSQAANVHSITHTTEYAAAOVIERLS 121

RESULT 4
US-09-771-383-1

Patent No. 6957150
GENERAL INFORMATION:
APPLICANT: Parris, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark

```

: TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
:
: TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
:
: FILE REFERENCE: 2368/12
:
: CURRENT APPLICATION NUMBER: US/09/771,383
:
: CURRENT FILING DATE: 2001-01-25
:
: PRIOR APPLICATION NUMBER: US 60/178,639
:
: PRIOR FILING DATE: 2000-01-28
:
: NUMBER OF SEQ ID NOS: 13
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 1
:
: LENGTH: 121
:
: TYPE: PRT
:
: ORGANISM: B. subtilis
:
US-09-771-383-1

```

Query Match	99.3%	Score 591;	DB 2;	Length 121;
Best Local Similarity	100.0%;	Pred. No. 2.5e-63;		
Matches 119;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2 YGIGLDITELKRIASNAGRKQFAERILTRSELDQYTELSEKKRKEFLGRIAAKEAFSK 61

Db 3 YGIGLDITELKRIASNAGRKQFAERILTRSELDQYTELSEKKRKEFLGRIAAKEAFSK 62

QY 62 AFGTGTGROLSFODIRKQNGKXPILCTKLSQAAVHLSITHTKEAANAQVITRLLSS 120

Db 63 AFGTGTGROLSFODIRKQNGKXPILCTKLSQAAVHLSITHTKEAANAQVITRLLSS 121

RESULT 5
US-09-771-383-11
; Sequence 11, Application US/09771383

```

# Patent No. 6957150
# GENERAL INFORMATION:
# APPLICANT: Parriss, Kevin
# APPLICANT: Somers, William
# APPLICANT: Tam, Amy
# APPLICANT: Lin, Laura
# APPLICANT: Stahl, Mark
# TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
# TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
# FILE REFERENCE: 2368/12
# CURRENT APPLICATION NUMBER: US/09/771,383
# CURRENT FILING DATE: 2001-01-25
# PRIOR APPLICATION NUMBER: US 60/178,639
# PRIOR FILING DATE: 2000-01-28
# NUMBER OF SEQ ID NOS: 13
# SOFTWARE: Patentin version 3.0
# SEQ ID NO 11
# LENGTH: 121
# TYPE: PRT
# ORGANISM: Bacillus
# US-09-771-383-11

```

Query Match	99.3%	Score 591	DB 2	Length 121
Best Local Similarity	100.0%	Pred. No. 2.5e-63		
Matches 119; Conservative	0	Mismatches	0	Indels 0; Gaps 0

Qy 2 YGIGLDITTEKRIASAMGRQKRFABEILITNESELDQYTELSEKKNQFLGKPAKKAFAFK 62

Db 3 YGIGLDITTEKRIASAMGRQKRFABEILITRSELDQYTELSEKKNQFLGKPAKKAFAFK 62

Qy 62 AFGTGTGIRQUSFQDIERKQNGKPPYITCKLSQAAMVHSITHTTKRYAAAQVIVIELLS 122

Db 63 AFGTGTGIRQUSFQDIERKQNGKPPYITCKLSQAAMVHSITHTTKRYAAAQVIVIELLS 122

RESULT 6

```

; Sequence 4274, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

```

TYPE: amino acid

```

?      TOPOLOGY: linear
?
?      MOLECULE TYPE: Protein
?
?      HYPOTHETICAL: YES
?      ORIGINAL SOURCE:
?      ORGANISM: Enterococcus faecium
?
?      FEATURE:
?      NAME/KEY: misc_feature
?      LOCATION: (B) LOCATION 1...129
?
?      SEQUENCE DESCRIPTION: SEQ ID NO: 6990:
?
?      US-09-107-532A-6990

```

Query Match	43.7%	Score 260;	DB 2;	Length 129;
Best Local Similarity	48.2%;	Pred. No. 1.8e-23;		
Matches	55;	Conservative	22;	Mismatches 35;
			Indels	2;
			Gaps	2

```
QY      3 GIGDLITELKRIASMAGRÖKRFAERILTRSELDYYELBEKKNEFLAGRFAAKEAFSKA 62
        |||:| || | : : ||||| : : : ||| ||| : |||||
Db     17 GIGDAVELPRITRLIEEKPFLARILTSDEMKLFÖSLBPFHROVEFLGGGYACKAEAFSKA 76
```

QY 63 FCGHIGRGLSFODIETRKDNGKPYICTKLSQLAAVHVSITHREKYAAQVIE 116
 :|||||:::|||||::|||:: |||||::|||::||
 Db 77 WGTGIGIK-VTFQDVBEILKNENGQP-VWTRSPHGNAWVSIETHNETAFQIIILE 128

RESULT 10
US-09-583-110-3157
; Sequence 3157, Application US/09583110

```

1 GENERAL INFORMATION:
2 APPLICANT: Lynn Doucette-Stamm et al.
3 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
4 TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
5 FILE REFERENCE: PATHO0-07A
6 CURRENT APPLICATION NUMBER: US/09/583,110
7 CURRENT FILING DATE: 2000-05-26
8 PRIOR APPLICATION NUMBER: US 09/107,433
9 PRIOR FILING DATE: 1998-06-30
10 PRIOR APPLICATION NUMBER: US 60/085,131
11 PRIOR FILING DATE: 1998-05-12
12 PRIOR APPLICATION NUMBER: US 60/051,553
13 PRIOR FILING DATE: 1997-07-02
14 NUMBER OF SEQ ID NOS: 5332

```

Query Match	40.8%	Score 243	DB 2	Length 120
Best Local Similarity	44.1%	Pred. No. 1.8e-21		
Matches 52; Conservative	25;	Mismatches 31;	Indels 10;	Gaps 3

QY 3 GIGDLITELKRISMAGROKRFARILTRSELDQVYELESKRKNFELAGRPAKAFAFSKA 62
| : | | | | : | : | : | | | : : : | : : | : | : | : | : | : | : | : | :
Db 4 GHGIDIBELASIESAVTRHGEFKRVLTAAOEMERFTSLGRGRÖLEYLAGWSAKAFASKA 63

QY 63 FGTGIGRQLSPQDIIRKDNQNGKPYYICTKLQA-----AVHVSITHTREYAAQVIE 116
||| : : ||| : : : ||| : : : ||| : : :
Db 64 MGTGISK-LGFQDLEVLNNERGARPY----FSQAPSGSKIMWISISHTQFVTLSVILE 115

RESULT 11.14-2
 US-08-987-144-2
 ; Sequence 2, Application US/08987144
 ; Patent No. 6060282
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Rostock Jr., Paul R.
 ; TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
 ; TITLE OF INVENTION: dpj-acps
 ;
 ; NUMBER OF SEQUENCES: 3
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Eli Lilly and Company
 ; STREET: Lilly Corporate Center
 ;

CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.

DATE: 10/26/83
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match	40.8%	Score 243;	DB 2;	Length 122;
Best Local Similarity	44.1%	Pred. No. 1.8e-21;		
Matches 52; Conservative	25;	Mismatches 31;	Indels 10;	Gaps 3;

QY 3 GIGDITELKRIASWAGROKRAIRILTRSELDQYELSEKRNIEFLAGRFAAKEAFSKA 622

Db 6 GGGIIEELMSIESAVTRHHEGAKRVULTAOEMERFTSLKGRQIEYLAGWSAKAEAFSKA 655

Qy 63 FGTGIGRQLSPDIEIRKQNGKYYICTKLSQA-----AVHVSITHTKEVAAQVIE 116
||| : | ||| : : | || : ||| : ||| : : ||| : : | : ||
Db 66 MGTGISK-LGFDLEVLNNRGAPY-----FSQAPSGKIMWISISHDQFVTSVILE 117

```

RESULT 12
US-09-163-446-2
; Sequence 2, Application US/09163446
; Patent No. 6515119
; GENERAL INFORMATION:
; APPLICANT: Fritze, Christian
; APPLICANT: Youngman, Philip
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
; FILE REFERENCE: 07334/097001
; CURRENT APPLICATION NUMBER: US/09/163,446
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Streptococcus pneumonia
US-09-163-446-2

```

Query Match	40.8%	Score 243;	DB 2;	Length 156;
Best Local Similarity	44.1%	Pred. No. 2.6e-21;		
Matches 52; Conservative	25;	Mismatches 31;	Indels 10;	Gaps 32.

```

QY      3 GIGDITELKRIASWAGROKREAFERILTRSELDQYELSEKKNIEFLAGRPAKAEAFSKA 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     40 GHGDIIEELSIESAATRHEGFPAKRVLTAEOMERFTSLKGRQLEYLAGWSAKAEAFSKA 99

```

```
Dy      63 FGTGIRQLSPDIEIRKDNQKPYYICTLSQA----AVHVSITHTEKYAAQVVE    116  
       |||| : | ||| : :: |||   ||| : : ||| : : ||| : :  
Db     100 MGTGISK-IGFDLEVLNNRGAPY-----FSOAPSCKIWNISISHDOFVTASVILE    151
```

```

FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7596
LENGTH: 138
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7596

Query Match
Best Local Similarity 41.1%; Pred. No. 2,3e-17;
Matches 51; Conservative 22; Mismatches 40; Indels 11; Gaps 4;

QY 3 GIGLDITELKRISMAGRO-KPAERILITRSELDQYELSEKRNKEFLAGPAAKEAFSK 61
Db 17 GIGMDIVELSRLEELIGRGGERLARILITDNEWMIYQ--SHKQPVRFIAKSPFAVEAAAK 74
62 ARGTGIGROLSFODIEIRKQNGKYI-----ICTLSQA---AVHSITHTKEVAAQV 113
Db 75 ALGTGIRLGIAFNHFVANDELGKPTLHFLAVAKEMAKAGINALHVTLADEQRYACATV 134
QY 114 VIER 117
Db 135 ILEK 138

RESULT 15
US-09-770-834-7
Sequence 7, Application US/09770834
Patent No. 6684162
GENERAL INFORMATION:
APPLICANT: Parriss, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
TITLE OR INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
FILE REFERENCE: 2366/14
CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 169
TYPE: PRT
ORGANISM: Thermotoga sp.
US-09-770-834-7

Query Match
Best Local Similarity 42.4%; Pred. No. 2.8e-16;
Matches 50; Conservative 23; Mismatches 30; Indels 15; Gaps 7;

QY 3 GIGDITELKRISMAGROKPAERILITRSELDQYELSEKRNKEFLAGPAAKEAFSK 62
Db 4 GVGIDIVELERV-----DEKFAERILGSEKRLF--LTRKRREFIAGRFPAKFAFFRA 55
63 FGFGIGROLSFODIEIRKQNGKPYIICTLSQA---AVHSITHTKEVAAQVYIER 117
Db 56 LGGTGINOH-SFTLYEF-LESNGKP-VLCYHKDGFNFVNAHVSLSHR-FAVALVLEK 109

Search completed: December 21, 2005, 13:55:50
Job time : 40.403 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:34 ; Search time 174.925 Seconds
(without alignments)
483.997 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
Sequence: 1 AYGIGLDITELKRIASMAGR.....SITHKEYAAQVIERLSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	99.3	121	1	ACPS_BACSU
2	334.5	56.2	129	1	ACPS_GEOKA
3	329.5	55.4	117	1	ACPS_BACSK
4	313	52.6	119	1	ACPS_BACR
5	304	51.1	119	1	ACPS_BACN
6	304	51.1	119	1	ACPS_BACHK
7	303	50.9	119	1	ACPS_BACCI
8	303	50.9	119	2	Q4MPT7_BACCE
9	300	50.4	119	1	ACPS_BACDZ
10	297	49.9	119	1	ACPS_BACD
11	287	48.2	118	1	ACPS_LISMF
12	287	48.2	118	1	ACPS_LISMO
13	283	47.6	118	1	ACPS_LISL
14	279.5	47.0	117	1	ACPS_STABP
15	279.5	47.0	117	1	ACPS_STABP
16	278.5	46.8	119	2	Q4LV66_STAHU
17	278	46.7	119	1	ACPS_STAC
18	278	46.7	119	1	ACPS_STRAU
19	277.5	46.6	119	1	ACPS_OCEIH
20	275	46.2	119	1	ACPS_STAM
21	275	46.2	119	1	ACPS_STAM
22	275	46.2	119	1	ACPS_STAM
23	275	46.2	119	1	ACPS_STAM
24	275	46.2	119	1	ACPS_STAM
25	269	45.2	117	1	ACPS_ENTFA
26	261	43.9	119	1	ACPS_LACPL
27	252.5	42.4	120	1	ACPS_LACPL
28	246.5	41.4	119	1	ACPS_LACRO
29	245	41.2	117	1	ACPS_LACRE
30	243	40.8	120	1	ACPS_STRPN
31	243	40.8	120	1	ACPS_STRK6

32	241.5	40.6	126	2	Q5E318_VIBF1
33	237.5	39.9	126	1	ACPS_VIBCH
34	237.5	39.2	126	1	ACPS_VIBU
35	231.5	38.9	126	1	ACPS_VIBV
36	228.5	38.4	118	2	Q5FM33_LACAC
37	228.5	38.4	119	1	ACPS_STR3
38	228.5	38.4	119	1	ACPS_STR5
39	227	38.2	119	1	ACPS_STRMU
40	227	38.2	119	2	Q5M2S6_STR12
41	227	38.2	119	2	ACPS_VIBPA
42	223.5	37.6	126	1	ACPS_CLOAB
43	221.5	37.2	124	1	ACPS_STRP3
44	221	37.1	118	1	ACPS_STRP6
45	221	37.1	118	1	ACPS_STRP6

ALIGNMENTS

RESULT 1
ACPS_BACSU STANDARD; PRT; 121 AA.
ID ACPS_BACSU
AC P96618;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-(acyl)-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)
GN Name=acps; OrderedLocustNames=BSU04620;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1423;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
RL Bacillus subtilis genome";
RN Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunze F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bartolo M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Dentzot F., Davine K.M., Duesterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Eutlan K.-D., Evington J., Fabre C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi E.J., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Gollightly E.J., Grand G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Kleeschard M.,
RA Klein C., Kobayashi Y., Koeter P., Koningsstein G., Krogh S.,
RA Krumo M., Kunita K., Lapidis A., Lardinois S., Laber U.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S.,
RA Nobak S., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Punelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger W., Rivolta C., Rocha E., Roche R.,
RA Rose M., Sadaie Y., Sato T., Scanlan A., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenhof M., Vannier F.,
RA Vasseroiti A., Viati A., Wambou R., Wedler B., Wedler H.,
RA Wellenreger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasunoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
RA Yoshikawa H., Zanchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus

RT subtilis.";
 RL Nature 390:249-256(1997).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=21463117; PubMed=11489886; DOI=10.1074/jbc.M103556200;
 RA Moez H.D., Finking R., Marahiel M.A.;
 RT "4'-phosphopantetheine transfer in primary and secondary metabolism of
 RT Bacillus subtilis.";
 RL J. Biol. Chem. 276:37289-37298(2001).
 RN [4]
 RP MUTAGENESIS OF ILE-2, ILE-5 AND GLN-113, AND X-RAY CRYSTALLOGRAPHY
 RP WITH HOLO-(ACYL CARRIER PROTEIN).
 RX Pubmed=10997907; DOI=10.1016/S0969-2126(00)00178-7;
 RA Paries K.D., Lin L., Tam A., Mathew R., Hixon J., Stahl M.,
 RA Fritz C.C., Seehra J., Somers W.S.;
 RT "Crystal structures of substrate binding to Bacillus subtilis holo-
 RT (acyl carrier protein) synthase reveal a novel trimetric arrangement of
 RT molecules resulting in three active sites.";
 RL Structure 8:883-895(2000).
 CC -I- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of fatty acid acyl-carrier protein ACP. Also modifies
 CC the D-lamyl carrier protein but fails to recognize PCP and acpP,
 CC an acyl carrier protein of secondary metabolism.
 CC -I- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -I- COFACTOR: Magnesium (By similarity).
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -I- SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
 CC family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AB001488; BA19299.1; -; Genomic DNA.
 CC EMBL; Z89106; CAB12269.1; -; Genomic DNA.
 CC PIR; H69772; H69772.
 CC DR PDB; 1F80; X-ray; A/B/C=-.
 CC DR Subtilist; BG12089; acps.
 CC DR HAMAP; MF_00101; -; 1.
 CC DR InterPro; IPR008278; 4-PPT_transf.
 CC DR InterPro; IPR002582; ACPs.
 CC DR InterPro; IPR004568; Pantethn_trans.
 CC DR Pfam; PF01648; ACPs; 1.
 CC DR ProDom; PD004282; ACPs; 1.
 CC DR TIGRFAMs; TIGR00516; acps; 1.
 CC DR TIGRFAMs; TIGR00556; pantethn_tm; 1.
 CC 3D-structure; Complete proteome; Fatty acid biosynthesis;
 CC Lipid synthesis; Magnesium; Metal-binding; Transferase.
 CC KW METAL 8 8
 CC FT METAL 58 58
 CC FT MUTAGEN 2 2
 CC FT MUTAGEN 5 5
 CC FT MUTAGEN 5 5
 CC FT MUTAGEN 5 5
 CC FT MUTAGEN 5 5
 CC FT STRAND 113 113
 CC FT MUTAGEN 113 113
 CC FT STRAND 2 11
 CC FT HELIX 12 21
 CC FT TURN 23 24
 CC FT TURN 25 29
 CC FT HELIX 32 38
 CC FT TURN 33 39
 CC FT TURN 39 40
 CC FT HELIX 43 64
 CC FT TURN 43 65
 CC FT TURN 65 65
 CC FT STRAND 69 69
 CC FT TURN 70 71
 CC FT STRAND 72 72
 CC FT STRAND 72 72
 CC FT HELIX 74 76

FT STRAND 78 81
 FT TURN 83 84
 FT STRAND 87 91
 FT TURN 92 94
 FT STRAND 95 105
 FT STRAND 109 117
 SQ SEQUENCE 121 AA; 13718 MW; 6C10401DA7116701 CRC64;
 Query Match 99.3%; Score 591; DB 1; Length 121;
 Best Local Similarity 100.0%; Pred. No. 5.2e-47;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YGIGDITELKRIISMAGROKRFARILITRESELDQYVELSEKRNELAGFAAKAFSK 61
 DB 3 YGIGDITELKRIISMAGROKRFARILITRESELDQYVELSEKRNELAGFAAKAFSK 62
 QY 62 AFGGIGRQLSFODIEIRKDNQKPYIITCTLSQAAVHVSITTTKEFYAAQVIERLSS 120
 DB 63 AFGGIGRQLSFODIEIRKDNQKPYIITCTLSQAAVHVSITTTKEFYAAQVIERLSS 121
 RESULT 2
 ID ACPs_GEOKA STANDARD; PRT; 129 AA.
 AC Q51JG7;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocustNames=GK0228;
 OS Geobacillus kaustophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxId=1462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=HTA426;
 RX Pubmed=15576355; DOI=10.1093/nar/gkh970;
 RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
 RA Matsui S., Uchiyama I.;
 RT "Thermoadaptation trait revealed by the genome sequence of
 RT thermophilic Geobacillus kaustophilus.";
 RL Nucleic Acids Res. 32:6292-6303(2004).
 CC -I- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC -I- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -I- COFACTOR: Magnesium (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -I- SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
 CC family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; BA000043; BAD74513.1; -; Genomic DNA.
 CC DR HAMAP; MF_00101; -; 1.
 CC DR InterPro; IPR008278; 4-PPT_transf.
 CC DR InterPro; IPR002582; ACPs.
 CC DR InterPro; IPR004568; Pantethn_trans.
 CC DR Pfam; PF01648; ACPs; 1.
 CC DR ProDom; PD004282; ACPs; 1.
 CC DR TIGRFAMs; TIGR00516; acps; 1.
 CC DR TIGRFAMs; TIGR00556; pantethn_tm; 1.
 CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 CC Magnesium; Metal-binding; Transferase.
 CC KW METAL 8 8
 CC FT METAL 58 58
 CC FT METAL 58 58
 CC FT SEQUENCE 129 AA; 14213 MW; 302421348F6526C CRC64;

Query Match 56.2%; Score 334.5; DB 1; Length 129;
 Best Local Similarity 60.3%; Pred. No. 3.5e-23;
 Matches 70; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

QY 3 GIGLIDITELKRIASMAAGROKFAERILITRSELDQYVELSEKRNKNEFLAGRFAKAFAFKA 62
 DB 4 GIGLIDIVELERIRSLERSKRPERILITPREKAQOGELPPARQAFLGRFAKAYAKA 63
 QY 63 FGTGIGRQSLFODIEIRKQNGKPYIITCKLSQAAMVHSITHTKXYAAQVIERL 118
 DB 64 LGTIGRHLSPFDIEIVSEHGKPSIAARQGE-ITVHISHSRDYAAQVIERL 118

RESULT 3
 ACPS_BACSK STANDARD; PRT; 117 AA.
 ID ACPS_BACSK STANDARD; PRT; 117 AA.

AC 05MAY1;
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps)
 GN Name=acps; OrderedLocNames=ABC0805;
 OS Bacillus cereus (strain KSM-K16)
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=66692;
 [1]
 RT NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Takaki Y., Kageyama Y., Shimamura S., Suuki H., Nishi S., Hatada Y.,
 RA Kawai S., Ito S., Horikoshi K.
 RT "The complete genome sequence of the alkaliphilic Bacillus clausii
 KSM-K16."
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; AP006627; BAD63344.1; -; Genomic_DNA.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantech_n_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantech_n_tm; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KM Magnesium; Metal-binding; Transferase.
 FT METAL 8 Magnesium (By similarity).
 FT METAL 58 Magnesium (By similarity).
 SQ SEQUENCE 117 AA; 12841 MW; 9389775ED4411A38 CRC64;

Query Match 55.4%; Score 329.5; DB 1; Length 117;
 Best Local Similarity 61.4%; Pred. No. 9.1e-23;
 Matches 70; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 3 GIGLIDITELKRIASMAAGROKFAERILITRSELDQYVELSEKRNKNEFLAGRFAKAFAFKA 62
 DB 4 GIGLIDITELKRIEAFARQPRFORVLTSEYQDQMAQLABNRQIEYLAGRFAKAFAFKA 63
 QY 63 FGTGIGRQSLFODIEIRKQNGKPYIITCKLSQAAMVHSITHTKXYAAQVIERL 116

DB 64 KGTGIGAGLSWHDIEIRTEGSKPYIVND-DSARVHLSTHSKXYAAQVIERL 116

RESULT 4
 ACPS_BACSK STANDARD; PRT; 119 AA.
 ID ACPS_BACSK STANDARD; PRT; 119 AA.
 AC 08117;
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps)
 GN Name=acps; OrderedLocNames=BC0262;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=226900;
 [1]

RT NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapralov V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis."
 RT Nature 423:87-91(2003).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; AE016998; AAP07331.1; -; Genomic_DNA.
 DR HSP; P96618; 1F7L.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantech_n_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantech_n_tm; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KM Magnesium; Metal-binding; Transferase.
 FT METAL 8 Magnesium (By similarity).
 FT METAL 58 Magnesium (By similarity).
 SQ SEQUENCE 119 AA; 13296 MW; 799459B3082D626B CRC64;

Query Match 52.6%; Score 313; DB 1; Length 119;
 Best Local Similarity 54.7%; Pred. No. 3.2e-21;
 Matches 64; Conservative 22; Mismatches 29; Indels 2; Gaps 1;

QY 3 GIGLIDITELKRIASMAAGROKFAERILITRSELDQYVELSEKRNKNEFLAGRFAKAFAFKA 62
 DB 4 GIGLIDITELKRIEAKMDGKLKEMERILITENERNVAMELGSRITFEVAGRFAKAFAFKA 63
 QY 63 FGTGIGRQSLFODIEIRKQNGKPYIITCKLSQAAMVHSITHTKXYAAQVIERL 119
 DB 64 VGTGIGKEVSLDIEVKDERGKPYIITLTS-TEYIVHLSHSKXYAAQVIERL 118

RESULT 5

ACPS_BACAN STANDARD; PRT; 119 AA.
 ID ACPS_BACAN Q6149; Q6K161;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Hololacetyl-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocustNames=Ba0250, GBA0250, BAS0236;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames / Isolate Porton;
 RX MEDLINE=2608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillye L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin H.M., Radune D.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Raddue D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria."
 RL Nature 423:81-86(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames / Isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RA "Bacillus anthracis comparative genomics."
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Stemne;
 RA Hitchcock P., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Richardson P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of Bacillus anthracis Stemne."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AE017024; AAP24289.1; -; Genomic DNA.
 CC EMBL: AE017334; AAT29331.1; -; Genomic DNA.
 CC EMBL: AE017225; AAT52572.1; -; Genomic DNA.
 CC HSSP: P96618; 1F7L.
 CC TIGR: BAO250; -.
 CC HAMAP: MF_00101; -; 1.
 CC InterPro: IPR008278; 4-PPT_transf.
 CC InterPro: IPR002582; ACPS.
 CC InterPro: IPR004568; Pantethn_trans.
 CC Pfam: PF01648; ACPS; 1.

DR ProDom: PD004282; ACPS; 1.
 DR TIGRFAMs: TIGR00516; acps; 1.
 DR TIGRFAMs: TIGR00556; pantethn_tm; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 FT METAL 8 8 Magnesium (By similarity).
 FT METAL 58 58 Magnesium (By similarity).
 SQ SEQUENCE 119 AA; 13100 MW; 8680A0B258813E14 CRC64;
 Query Match 51.1%; Score 304; DB 1; Length 119;
 Best local Similarity 54.2%; Pred. No. 2.2e-20;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;
 QY 3 GIGDITELKRIASMAKQKRFARITRSELDQYELSEKSKKPEFLAGRAKAEAFSA 62
 DB 4 GIGDITELNRIEKLQKLGKFMERILITENRNVAKLQKSRLLTEFVAGRFPAKEATSKA 63
 QY 63 FGTSIGRQLSPQDIEIRKONGKPEYIITKLSQAAVHSVITHTKYVAAQVIERLSS 120
 DB 64 VGTGIGKEVSFLDIEVRNDRGKRLITS--TEHIVLSISHSKFAVAQVLESSSS 119
 RESULT 6
 ACPS_BACHK STANDARD; PRT; 119 AA.
 ID ACPS_BACHK Q6HBE3;
 AC 06HBE3;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Hololacetyl-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocustNames=Br9727_0222;
 OS Bacillus thuringiensis (subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=180856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=97-27;
 RA Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of Bacillus thuringiensis 97-27."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AE017355; AAT62521.1; -; Genomic DNA.
 CC HAMAP: MF_00101; -; 1.
 CC InterPro: IPR008278; 4-PPT_transf.
 CC InterPro: IPR002582; ACPS.
 CC InterPro: IPR004568; Pantethn_trans.
 CC Pfam: PF01648; ACPS; 1.
 CC ProDom: PD004282; acps; 1.
 CC TIGRFAMs: TIGR00516; acps; 1.
 CC TIGRFAMs: TIGR00556; pantethn_tm; 1.
 CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 KW METAL 8 8 Magnesium (By similarity).
 KW METAL 58 58 Magnesium (By similarity).
 FT SEQUENCE 119 AA; 13100 MW; 8680A0B258813E14 CRC64;

Query Match 51.1%; Score 304; DB 1; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.2e-20;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

DB 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 62
 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 120
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 119

QY 3 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 62
 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 63

DB 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 120
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 119

RESULT 7
 ACPS_BACCI STANDARD; PRT; 119 AA.
 ID ACPS_BACCI STANDARD; PRT; 119 AA.
 AC Q73ET8;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 GN Name=acps; OrderedLocustNames=BC0270;
 OS Bacillus cereus (strain ATCC 10987);
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 NX NCBI_TaxID=222523;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiolini S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 adaptations and a large plasmid related to *Bacillus anthracis* pXO1."
 RL Nucleic Acids Res. 32:977-988(2004).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AE017264; MAS39206.1; -; Genomic_DNA.
 DR TIGR; BCE0270; -;
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS_
 DR InterPro; IPR004568; Pantethn_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KM Magnesium; Metal-binding; Transferase.
 FT METAL 8 Magnesium (By similarity).
 FT METAL 8 Magnesium (By similarity).
 SQ SEQUENCE 119 AA; 13142 MW; 4AAA47DE92815CDC CRC64;

Query Match 50.9%; Score 303; DB 1; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.7e-20;
 Matches 64; Conservative 19; Mismatches 32; Indels 2; Gaps 1;

QY 3 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 62

DB 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 63
 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 118

QY 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 118

DB 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 118

RESULT 8
 Q4MPT7_BACCE PRELIMINARY; PRT; 119 AA.
 ID Q4MPT7_BACCE PRELIMINARY; PRT; 119 AA.
 AC Q4MPT7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7).
 GN Name=acps; ORFNames=BC_G9241_0240;
 OS Bacillus cereus G9241.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 NX NCBI_TaxID=269801;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G9241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Malden M.C.J., Priest F.G., Barker W., Jiang L., Cer R.Z.,
 RA Ristone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identification of anthrax toxin genes in a *Bacillus cereus* associated
 RT with an illness resembling inhalation anthrax."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AE0100017; E014228.1; -; Genomic_DNA.
 KM Transferase.
 SQ SEQUENCE 119 AA; 13142 MW; 0B16DAE95812BDB CRC64;

Query Match 50.9%; Score 303; DB 2; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.7e-20;
 Matches 64; Conservative 19; Mismatches 32; Indels 2; Gaps 1;

QY 3 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 62
 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 63

DB 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKNEFLGFAKFAKAFSKA 63
 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 118

QY 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 118

DB 63 FTGTGIGROLSFODIEIRKQNGKPYIICTKLSQAAVHSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVLESSSS 118

RESULT 9
 ACPS_BACCC STANDARD; PRT; 119 AA.
 ID ACPS_BACCC STANDARD; PRT; 119 AA.
 AC Q63GX2;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] transferase (acps).
 GN Name=acps; OrderedLocustNames=BCZK0224;
 OS Bacillus cereus (strain ZK).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 NX NCBI_TaxID=286681;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus cereus* ZK."

```

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR HAMAP, CP000001; AAU20010.1; -; Genomic_DNA.
CC DR HAMAP, MF_00101; -; 1.
CC DR InterPro: IPR008278; 4-PPT_transf.
CC DR InterPro: IPR002582; ACPS_trans.
CC DR InterPro: IPR004568; Pantethn_trans.
CC DR Pfam: PF01648; ACPS; 1.
CC DR ProDom: PD004282; ACPS; 1.
CC DR TIGRFAMs: TIGR00516; acps; 1.
CC DR TIGRFAMs: TIGR00556; pantethn_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferrase.
CC METAL 8 Magnesium (By similarity).
CC METAL 8 Magnesium (By similarity).
CC FT METAL 8 Magnesium (By similarity).
CC SQ SEQUENCE 119 AA; 13169 MW; 8730A0B258813E14 CRC64;

Query Match 50.4%; Score 300; DB 1; Length 119;
Best Local Similarity 53.8%; Pred. No. 5.1e-20;
Matches 63; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

QY 3 GIGLDITELKRIASMAGROKRFARILTRSELDQYVEISEKRNKEFLAGRFAKSAFSA 62
DB 4 GTGIDIVELRIQGMVHEKHPFVKKILTENQGEVFAVLSRRRLREYIAGRFAKSAFSA 63
QY 63 FGTGIGRQLSFODIEIRKQNGKPYIITCKLSQAAYVSTHTKXYAAQVIVIRLS 119
DB 64 VGTGIGKEVSPDIEVRNDRGKPIILITS--TEHIVHLSHSKKEFAVAQVIVIRLS 118

RESULT 10
ACPS_BACBD STANDARD; PRT; 119 AA.
AC Q9KFG1;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=BH0518;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=8665;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RT Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

```

```

CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR EMBL, BA000004; BAB04237.1; -; Genomic_DNA.
CC DR PIR, F83714; F83714.
CC DR HSSP, Q9FTT5; 1PTH.
CC DR HAMAP, MF_00101; -; 1.
CC DR InterPro: IPR008278; 4-PPT_transf.
CC DR InterPro: IPR002582; ACPS_trans.
CC DR InterPro: IPR004568; Pantethn_trans.
CC DR Pfam, PF01648; ACPS; 1.
CC DR ProDom, PD004282; ACPS; 1.
CC DR TIGRFAMs: TIGR00516; acps; 1.
CC DR TIGRFAMs: TIGR00556; pantethn_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferrase.
CC METAL 8 Magnesium (By similarity).
CC METAL 8 Magnesium (By similarity).
CC FT METAL 8 Magnesium (By similarity).
CC SQ SEQUENCE 119 AA; 13421 MW; 2279B552549041C9 CRC64;

Query Match 49.9%; Score 297; DB 1; Length 119;
Best Local Similarity 50.0%; Pred. No. 9.6e-20;
Matches 59; Conservative 25; Mismatches 32; Indels 2; Gaps 2;

QY 3 GIGLDITELKRIASMAGROKRFARILTRSELDQYVEISEKRNKEFLAGRFAKSAFSA 62
DB 4 GTGIDIVELRIQGMVHEKHPFVKKILTENQGEVFAVLSRRRLREYIAGRFAKSAFSA 63
QY 63 FGTGIGRQLSFODIEIRKQNGKPYIITCKLSQAAYVSTHTKXYAAQVIVIRLS 120
DB 64 VGTGISAEGVHWDLEIVSDERKRP-VLSVNL-DATIHVSISHSOSYAIAQVIVIRLS 119

RESULT 11
ACPS_LISMF STANDARD; PRT; 118 AA.
AC Q721T0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=LM02365_0904;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_Taxid=265669;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Raeko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forrester H.A., Tran B., Katharopoulos S., Whorlitz L.D., Whittich G.A.,
RA Bayles D.O., Luchaneky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species.";
RT Nucleic Acids Res. 32:2386-2395(2004).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps

```

```
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE017325; AAT03684.1; -; Genomic_DNA.
CC TIGR; LMOF2365.0904; -.
CC HAMAP; MF_00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPs.
CC InterPro; IPR004568; Pantech_n_trans.
CC Pfam; PF01648; ACPs; 1.
CC ProDom; PD004282; ACPs; 1.
CC TIGRPFAM; TIGR00516; acps; 1.
CC TIGRPFAM; TIGR00556; pantech_n_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC METAL 8 8 Magnesium (By similarity).
CC FT METAL 58 58 Magnesium (By similarity).
CC SQ SEQUENCE 118 AA; 13257 MW; 5584C5C769181B3F CRC64;

Query Match 48.2%; Score 287; DB 1; Length 118;
Best Local Similarity 50.9%; Pred. No. 8.1e-19;
Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 GIGLITTELKRIASMGQKRFARILITRSELDQYVEISEKKNEFLAGFAKAEAFSKA 62
DB 4 GIGLMDIERKQVQVEKPRFIERVLTKEIKQFEKYEGRNKRIFELAGFAKAEAFSKA 63
DB 64 NGTGFGKHSFTFVDEILQVEDGRPHVTLPVKSGENFVSITHTAPSAQAQVIE 117

RESULT 12
ACPS LISMO STANDARD; PRT; 118 AA.
AC 08y8t2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 13-SBP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocNames=lm00885;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruhnok C., Amend A.,
BAguero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Ertian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```

```
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL159197; CAC98963.1; -; Genomic_DNA.
CC PIR; AB1185; AE1185.
CC HSSP; P96618; 1F7L.
CC ListerList; LMO00885; -.
CC HAMAP; MF_00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPs.
CC InterPro; IPR004568; Pantech_n_trans.
CC Pfam; PF01648; ACPs; 1.
CC ProDom; PD004282; ACPs; 1.
CC TIGRPFAM; TIGR00516; acps; 1.
CC TIGRPFAM; TIGR00556; pantech_n_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC METAL 8 8 Magnesium (By similarity).
CC FT METAL 58 58 Magnesium (By similarity).
CC SQ SEQUENCE 118 AA; 13257 MW; 5584C5C769181B3F CRC64;

Query Match 48.2%; Score 287; DB 1; Length 118;
Best Local Similarity 50.9%; Pred. No. 8.1e-19;
Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 GIGLITTELKRIASMGQKRFARILITRSELDQYVEISEKKNEFLAGFAKAEAFSKA 62
DB 4 GIGLMDIERKQVQVEKPRFIERVLTKEIKQFEKYEGRNKRIFELAGFAKAEAFSKA 63
DB 64 NGTGFGKHSFTFVDEILQVEDGRPHVTLPVKSGENFVSITHTAPSAQAQVIE 117

RESULT 13
ACPS LISIN STANDARD; PRT; 118 AA.
AC 092DD0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SBP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocNames=lm00884;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruhnok C., Amend A.,
BAguero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Ertian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
```

CC	-!	SIMILARITY:	Belongs to the P-Pant transferase superfamily. Acps family.
CC			
CC	This	Swiss-Prot entry	is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC			
CC	EMBL;	AB016749; AAC005274.1; -;	Genomic_DNA.
DR	HSSP;	P96618; 1F7L.	
DR	HAMAP;	MF_00101; -;	1.
DR	InterPro;	IPIR008278; 4-PPT_transf.	
DR	InterPro;	IPIR005582; ACPS_trans.	
DR	InterPro;	IPIR004568; Pantectm_trans.	
DR	Pfam;	PF01648; ACPS; 1.	
DR	ProdDom;	PD004282; ACPS; 1.	
DR	TIGRFAMS;	TIGR00516; acps; 1.	
DR	TIGRFAMS;	TIGR00556; pantectm_tm; 1.	
KW	Complete	proteome; Fatty acid biosynthesis; Lipid synthesis; Magnesium; Metal-binding; Transferase.	
FT	METAL	8	Magnesium (By similarity).
FT	METAL	58	Magnesium (By similarity).
SO	SEQUENCE	117 AA; 13535 MW; 515246BC1C4DDED9 CRC64;	
Query Match		Best Local Similarity	47.0%; Score 279.5; DB 1; Length 117; Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;
Oy	2	YIGLDITTEKRIKSMAGROKFEAFRLT--BSELDQYYELSEKRNKEFLAGFAAKA	58
Dd	3	YGIDIDIEIERINGLQ-NOTKFRLETLTBENDKNGY--THEQRLEFLAGFYTKEA	59
Oy	59	FSKAFTGFGIGRGSLSFODIEIRKDQNGKPYYICTKLSPAAVHSITHTKETAADVIER	117
Dd	60	FSKALGTGLGKSVSFDINCYNDAIGRP--CIDYPGYTHVSTHTENYAMSGVILEK	115
RESULT 15			
ID	ACPS_STAEQ	STANDARD;	PRT; 117 AA.
AC	OSHMED4:		
DT	13-SEP-2005	(Rel. 48, Created)	
DT	13-SEP-2005	(Rel. 48, Last sequence update)	
DT	13-SEP-2005	(Rel. 48, Last annotation update)	
DE	HoLo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (HoLo-ACP synthase)		
DN	Name=acps; OrderedlocusNames=SER1684;		
OS	Staphylococcus epidermidis (strain ATCC 35984 / RP62a).		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=176279;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RX	PubMed15774886; DOI=10.1128/JB.187.7.2426-2438.2005;		
RA	Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T., Ravel J., Paulsen I.T., Kolonay J.F., Binkac L.M., Beanan M.J., Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S., Haft D.H., Vamathevan J.J., Khouri H., Uitterback T.R., Lee C., Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H., Hance I.R., Nelson K.E., Fraser C.M.;		
RT	"Insights on evolution of virulence and resistance from the complete genome analysis of an early methicillin-resistant Staphylococcus aureus strain and a biofilm-producing methicillin-resistant Staphylococcus epidermidis strain."		
RL	J. Bacteriol. 187:2426-2438(2005).		
CC	-!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (by similarity).		
CC	-!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl-carrier protein].		
CC	-!- COFACTOR: Magnesium (By similarity).		
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).		
CC	-!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.		

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----

DR EMBL; CP000029; AAM55047.1; -; Genomic_DNA.
 DR TIGR; SERP1684; -.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004368; Panethm_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRPFAM; TIGR00516; acps; 1.
 DR TIGRPFAM; TIGR00556; panethm_tm; 1.
 KW Complete proteome; Fatty acid_biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 FT METAL 8 8 Magnesium (By similarity).
 FT METAL 58 58 Magnesium (By similarity).
 SQ SEQUENCE 117 AA; 13535 MW; 515246BC1C4EDC9 CRC64;

Query Match 47.0%; Score 279.5; DB 1; Length 117;
 Best Local Similarity 51.3%; Pred. No. 4e-18;
 Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;

QY 2 YGIGLITELKRIASMAAGROKRPFAIRILT--RSELDQYVELSEKRNKEFLAGRFAPKEA 58
 DB 3 YGIGLITELKRIKLNQ-NQTKFIERILITEERDKLNQ--THEQRLEFLAGRFVKEA 59
 QY 59 FSKAFGTGIGRQLSPQDIEIRKDQNGKPYIICTKLSQAAVHSITHTKEYAAQVIER 117
 DB 60 FSKALGTGIGKSVSPQDINCYNDAIGKP--CIDYPGFTYHVSITHTENYAMSQVILEK 115

Search completed: December 21, 2005, 13:54:39
 Job time : 175.925 secs

This page blank (uspto)

This page blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:44 ; Search time 15.5224 Seconds
(without alignments)
743.830 Million cell updates/sec

Title: US-10-717-138-2

Sequence: 1 AYGLGIDITELKRIASMAGR.....SITHTKXYAAAVIERLSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	591	99.3	121	1	H69772	holo-[acyl]-carrier
2	297	49.9	119	2	F83714	holo-[acyl]-carrier
3	287	48.2	118	2	AE1185	holo-acyl-carrier
4	283	47.6	118	2	AD1543	holo-acyl-carrier
5	275	46.2	119	2	E89999	holo-ACP synthase
6	261	43.9	119	2	C86730	acyl-carrier prote
7	243	40.8	120	2	H95197	holo-[acyl]-carrier
8	243	40.8	120	2	D98064	holo-[acyl]-carrier
9	237.5	39.9	126	2	F82072	holo-[acyl]-carrier
10	221.5	37.2	124	2	B96960	holo-acyl-carrier
11	201.5	33.9	169	2	B72345	holo-[acyl]-carrier
12	201	33.8	126	2	F71662	holo-[acyl]-carrier
13	200.5	33.7	126	2	AF0356	holo-[acyl]-carrier
14	195.5	32.9	126	2	E91057	hypothetical protel
15	192.5	32.4	126	2	B85902	hypothetical protel
16	192.5	32.4	126	2	AG0828	holo-[acyl]-carrier
17	189.5	31.8	126	1	B42294	holo-[acyl]-carrier
18	189	31.8	131	2	A87810	hypothetical protel
19	188.5	31.7	126	2	F84959	holo-[acyl]-carrier
20	180.5	30.3	119	2	C71556	holo-[acyl]-carrier
21	178.5	30.0	125	2	D81833	holo-[acyl]-carrier
22	177.5	29.8	122	2	A86530	acyl-carrier protel
23	177.5	29.8	122	2	B72093	acyl-carrier protel
24	173.5	29.2	125	2	D81710	holo-[acyl]-carrier
25	173	29.1	125	2	F71276	holo-[acyl]-carrier
26	168.5	28.3	125	2	F81197	holo-[acyl]-carrier
27	166.5	28.0	119	1	H64620	holo-[acyl]-carrier
28	162.5	27.3	191	1	AC3413	holo-[acyl]-carrier
29	161.5	27.1	119	2	G71894	holo-[acyl]-carrier

30	158.5	26.6	134	2	H97485	holo-acyl-carrier
31	158.5	26.6	134	2	AH2703	holo-[acyl]-carrier
32	151	25.4	123	2	T35573	probable holo-acyl
33	139.5	23.4	133	2	B87442	holo-[acyl]-carrier
34	134.5	22.6	122	2	G85649	probable acyl-carrier
35	134.5	22.6	122	2	D90789	probable holo-acyl
36	133	22.4	133	2	F75544	holo-acyl-carrier
37	132.5	22.3	124	2	B70101	holo-acyl-carrier
38	132	22.2	115	2	A81286	probable holo-acyl
39	129.5	21.8	122	2	H70370	holo-[acyl]-carrier
40	127.5	21.4	115	2	G82895	holo-acyl-carrier
41	124	20.8	1857	1	S01787	fatty-acid synthase
42	115	19.3	130	2	B87058	holo-[acyl]-carrier
43	115	19.3	130	2	H70870	holo-[acyl]-carrier
44	113	19.0	1885	1	JC4086	fatty-acid synthase
45	104	17.5	119	1	S73864	hypothetical prote

ALIGNMENTS

```
RESULT 1
H69772 holo-[acyl]-carrier-protein] synthase (EC 2.7.8.7) - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: H69772
R:Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berber
C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Galler
A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
A.; Kestler, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapide, A.; Lardinois,
A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sekowaka, A.; Serox
A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
T.; Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A63580; MUID:98044033; PMID:9384377
A:Accession: H69772
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-121 <KUN>
A:Molecule type: DNA
A:Residues: 1-121 <KUN>
A:Cross-references: UNIPROT:P96618; UNIPARC:UP1000005FF70; GB:Z99106; GB:AL009126; NID:
A:Experimental source: strain 168
C:Genetics:
A:Gene: ydcB
C:Superfamily: holo-ACP synthase
C:Keywords: coenzyme A; transferase

Query Match 99.3%; Score 591; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. 4.8e-52;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGIGDITELKRIASMAGRKFAERILTRSEIDQYELSEKRNKEFLAARPAKAFSK 61
DB 3 YGIGDITELKRIASMAGRKFAERILTRSEIDQYELSEKRNKEFLAARPAKAFSK 62
OY 62 ARGTGIGRQLSFODIRIRNDQNGKPYITCTKLSQAANVHSITHTKXYAAAVIERLSS 120
DB 63 ARGTGIGRQLSFODIRIRNDQNGKPYITCTKLSQAANVHSITHTKXYAAAVIERLSS 121

RESULT 2
F83714 holo-[acyl]-carrier-protein] synthase BH0518 [imported] - Bacillus halodurans (strain C-1
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F83714
```

R,Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiraoka, Y. *Nucleic Acids Res.* 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: AB3650; MUID:20512582; PMID:11058132

A:Accession: F83714

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-119 <STD>

A:Cross-references: UNIPROT:Q9KEG1; UNIPARC:UPI0000125327; GB:AF001508; GB:BA000004; NITE:

A:Experimental source: strain C-125

C:Genetic8:

A:Gene: BH0518

A:Superfamily: holo-ACP synthase

	Query Match	49.9%;	Score 297;	DB 2;	Length 119;
	Best Local Similarity	50.0%;	Pred. No. 1.2e-32;		
	Matches	Conservative 25;	Mismatches 32;	Indels 2;	Gaps 2.
Oy	3	GIGDITELKRIASNAAGROKRAERILTRSELDÖYVELSEKKNFELGAPAKAEFSKA	62		
		: : : : : : : : : : :			
Db	4	GTGDIVELERIQSNVEKHPFVKILITENEQEVFARLSRRRLRYIAGRFAPAKAEFYKA	63		
Oy	63	FGTGGRLQSPDIDIRKQDQNGKPYITCTKLSQAANVHSITTKRYKAAQAVIIEELSS	120		
		: : : : : : : : : :			
Db	64	VGTGISABYGWMDIVLSDERKGP-VLSVNL-DATIHSHISQSYAIAQVILLERLSS	119		

RESULT 3
 AE1185
 holo-acyl-carrier protein synthase homolog lmo0885 [imported] - *Listeria monocytogenes* (C)Species: *Listeria monocytogenes*
 C.Date: 27-Nov-2001 #sequenceRevision 27-Nov-2001 #text_change 09-Jul-2004
 C.Accession: AE1185
 R.Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloekerker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H. D.; Jones, L.M.; Karet, U.
 Science 294, 849-852, 2001
 A.Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurupkat, G.; Madueno, E.; Maitournam, A.; McKee, C.; Schlueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
 A.Title: Comparative genomics of *Listeria* species.
 A.Reference number: AB1077; MUID:21537279; PMID:11679669
 A.Accession: AE1185
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-118 <GLA>
 A.Cross-references: UNIPROT:O8V8L2; UNIPARC:UP10000054DAF; GB:NC_003210; PIDD:CA698963.1
 A.Experimental source: strain EGD-e
 C.Genetics:
 A.Gene: lmo0885
 C.Superfamily: holo-ACP synthase

[illegible]

```

RESULT 4
AD1543
holo-acyl-carrier protein synthase homolog lin0894 [imported] - Listeria innocua (strain
C.Species: Listeria innocua
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Accession: AD1543
R.Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshl, H
D.; Jones, L.M.; Karst, U.

```

Science 294, 849-852, 2001
A:Authors: Krefetz, J.; Kuhn, M.; Kunst, F.; Kurapkát, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlutener, T.; Simoes, N.; Tlterrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1543
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-118 <G1A>
A:Cis86-references: UNIRROT-Q92DD0; UNIPARC:UP10000125338; GB:AL592022; PIDN:CAC96116.1;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0884
C:Superfamily: holo-ACP synthase

	Query Match	47.6%;	Score 283; DB 2;	Length 118;
	Best Local Similarity	51.3%;	Pred. No. 3,Je-21;	
	Matches	59;	Mismatches 39;	Indels 0; Gaps 0;
CY	3 GIGDITIELKRIASMAGRQKRFAIRILITRSLDDPYELSEKKNIIEFLAGRAAATASKA	62		
Dd	4 GIGDMIDLDLRVKAQVENPRFIERIILTETKETQYEKGESRKIEFLAGRAAAEAYAKA	63		
CY	63 FGTGIGROLSTODLEIKRDQNQRKYILLCTLSQAANVSITHTEVAANAQIVIER	117		
Dd	64 NGTFGGKLSTDEAILQVEDGRPHVMPIKOGFTVNSLTHTRASAQAQTIIQQ	118		

RESULT 5
 E89999
 holo-ACP synthase [imported] - Staphylococcus aureus (strain N315)
 C|Species: Staphylococcus aureus
 C|Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C|Accession: E89999
 R|Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Iji, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kato, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 lancet 357, 1235-1240, 2001
 A|Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A|Reference number: A89758; MUID:21311952; PMID:11418146
 A|Accession: E89999
 A|Status: Preliminary
 A|Molecule type: DNA
 A|Residues: 1-119 <KUR>
 A|Cross-references: UNIPROT:Q9NS14; UNIPARC:UP10000125346; GB:BA000018; P
 A|Experimental source: strain N315
 C|Genetics:
 A|Gene: dpj
 C|Superfamily: holo-ACP synthase

[illegible]

RESULT 6
C66730
acyl carrier protein synthase [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL14
C.Species: *Lactococcus lactis* subsp. *lactis*
C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_09-Jul-2004
C.Accession: C66730
R.Bolotin, A.; Wincker, P.; Manger, S.; Taillon, O.; Malarme, K.; Weisenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A.Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
A.Reference number: A86625; MUID:21235186; PMID:11337471

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:03 ; Search time 158.806 Seconds
(without alignments)
332.012 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
Sequence: 1 AVGIGLDITELKRIASWAGR.....SITHTKEYAAAVIERLSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	100.0	120	5 AAU010694	Aau10694 B. subtil
2	591	99.3	121	3 AAY88389	Aay88389 B-ydcb es
3	591	99.3	121	4 AAM52130	Aam52130 Bacillus
4	304	51.1	119	6 ABU18305	Abu18305 Protein e
5	287	48.2	118	5 ABR847581	Abb47581 Listeria
6	287	48.2	118	6 ABU32572	Abu32572 Protein e
7	281.5	47.3	124	5 ABP39429	Abp39429 Staphyloc
8	281.5	47.3	124	8 ADS04560	Ads04560 Staphyloc
9	279.5	47.0	117	6 ABU42933	Abu42933 Protein e
10	278.5	46.8	119	6 ABU43645	Abu43645 Protein e
11	278	46.7	119	6 ABR83238	Abt83238 S. aureus
12	278	46.7	119	6 ABM71799	Abm71799 Staphyloc
13	277	46.6	119	4 AAU33845	Aau33845 Staphyloc
14	277	46.6	119	4 AAU36808	Aau36808 Staphyloc
15	275	46.2	119	3 AAB14979	Aab14979 Staphyloc
16	275	46.2	119	6 ABU16272	Abu16272 Protein e
17	275	46.2	119	6 ADW94782	Adw94782 Prolifera
18	274	46.1	119	6 ABR83235	Abt83235 S. aureus
19	269	45.2	117	6 ABU29452	Abu29452 Protein e
20	269	45.2	117	8 ADH97041	Adh97041 E. faecal
21	269	45.2	117	8 ADH97039	Adh97039 E. faecal
22	269	45.2	117	8 AEC13396	Aec13396 Enterococ
23	269	45.2	117	9 AEC13394	Aec13394 Enterococ
24	267	44.9	117	4 AAU35183	Aau35183 Enterococ

25	262	44.0	126	6 ABU24470	Abu24470 Protein e
26	261	43.9	119	5 ABB54157	Abb54157 Lactococ
27	260	43.7	129	7 ADC97363	Adc97363 E. faeciu
28	250	42.0	117	6 ADB06134	Adb06134 Alloiococ
29	250	42.0	117	8 ADJ27057	Adj27057 Alloiococ
30	244	41.0	113	6 ADB06132	Adb06132 Alloiococ
31	243	40.8	120	3 AAY58607	Aay58607 Streptoco
32	243	40.8	120	6 ABU02175	Abu02175 S. pneumo
33	243	40.8	120	6 ABU46200	Abu46200 Protein e
34	243	40.8	120	6 ADK46642	Adk46642 Streptoco
35	243	40.8	122	2 AAW80612	Aaw80612 S. pneumo
36	243	40.8	122	4 AAU37879	Aau37879 Streptoco
37	243	40.8	122	4 AAU38056	Aau38056 Streptoco
38	243	40.8	122	7 ADB37480	Adb37480 S. pneumo
39	243	40.8	123	6 ABR83307	Abt83307 S. pneumo
40	243	40.8	123	6 ABR83308	Abt83308 S. pneumo
41	243	40.8	156	3 AAY88388	Aay88388 S-ydcb es
42	243	40.8	157	8 ADR95564	Adt95564 Novel S.
43	243	40.8	157	9 AEA59434	Aea59434 Streptoco
44	237.5	39.9	126	6 ABU49557	Abu49557 Protein e
45	228.5	38.4	119	3 AAY91289	Aay91289 Group B S

ALIGNMENTS

RESULT 1
AAU10694
ID AAU10694 standard; protein; 120 AA.
XX
XX
AC AAU10694;
DT 25-FEB-2002 (first entry)
DE
XX B. subtilis ACPs used to grow ACP/ACPS complex crystals.
XX
XX Crystal structure; acyl carrier protein synthase; acyl carrier protein;
KW rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-pant;
KM ACP/ACPS complex; protein co-ordinate data.
XX
XX Bacillus subtilis.
OS
XX
XX MO200185743-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 26-JAN-2001; 2001WO-0202949.
PR 08-MAY-2000; 2000US-0202466P.
XX
XX (AMHP) AMERICAN HOME PROD CORP.
PA (MILL-) MILLENNITUM PHARM INC.
XX
XX Pariss KD, Somers WS, Tam AS, Lin LT, Stahl ML, Powers R, Xu G;
WPI, 2002-055580/07.
XX
XX Crystallized complex useful in rational drug design methods, comprises
PT acyl carrier protein synthase and acyl carrier protein.
PS
XX Example 1; Fig 1; 147pp; English.
XX
XX The present invention relates to a crystallised structure comprising acyl
CC carrier protein synthase (ACPS) complexed with acyl carrier protein
CC (ACP). The invention also describes the solution structure of Bacillus
CC subtilis ACP. Both these structures are useful in rational drug design
CC methods for identifying agents that may interact with active sites of
CC ACPs and ACP, and for testing these agents to identify agents that may
CC represent novel antibiotics. They are also useful for design and
CC selection of potent and selective agents which interact with ACPs and
CC ACP, and for the design of antibiotics and other agents that interfere
CC with 4'-phosphopantetheinyl (P-pant) attachment, thus preventing
CC activation of corresponding carrier proteins. The present sequence

CC represents B. subtilis ACPS used to grow ACP/ACPS complex crystals
XX
SQ Sequence 120 AA;

Query Match 100.0%; Score 595; DB 5; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 60
DB 1 AVGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 60
QY 61 KAFGTGIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITHTKEYAAAQVIERLSS 120
DB 61 KAFGTGIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITHTKEYAAAQVIERLSS 120

RESULT 2
AAV88389
ID AAV88389 standard; protein; 121 AA.
XX
AC AAV88389;
XX
DT 25-JUL-2000 (first entry)
XX
DE B-ydcb essential bacterial protein amino acid sequence.

XX Bacterial gene; B-ydcb; Streptococcus pneumoniae; antibacterial compound;
KW acyl carrier protein synthase; identify; bacterial infection; treatment.
XX
OS Bacillus subtilis.
XX
FN WO200018952-A1.

XX 06-APR-2000.
XX
PD 30-SEP-1999; 99WO-US022666.
XX
PF 30-SEP-1998; 98US-00163446.
XX
PR (MILL-) MILLENNIUM PHARM INC.

XX Fritz C, Youngman P, Guzman L,
XX
XX WPI; 2000-303457/26.
XX
DR N-PSDB; AAA13271.

PT Identifying new antibacterial agents particularly against Streptococcus
PT pneumoniae, uses S-ydcb polypeptide from S. pneumoniae and B-ydcb
PT polypeptide from Bacillus subtilis.
XX
PS Claim 17; Fig 2; 58pp; English.

CC This sequence represents the essential bacterial protein B-ydcb from
CC Bacillus subtilis. B-ydcb is an ortholog of the S-ydcb from Streptococcus
CC pneumoniae. The gene encodes a protein which has structural
CC characteristics of acyl carrier protein synthase and displays synthase
CC activity in vitro. The protein is used in a method for identifying an
CC antibacterial agent, which comprises contacting an S-ydcb or B-ydcb
CC polypeptide with a test compound and detecting an interaction between the
CC polypeptide and the test compound, where the interaction indicates that
CC the compound is an antibacterial compound. Antibacterial agents
CC identified using the method may be used to treat a bacterial infection,
CC especially Streptococcus pneumoniae in mammals, especially a human or
CC rodent. The method can be configured for high throughput screening of
CC numerous candidate antibacterial agents, and identified agents should
CC have a broad spectrum of antibacterial activity

XX Sequence 121 AA;

Query Match 99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 61
DB 3 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 62
QY 62 AFGTIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITHTKEYAAAQVIERLSS 120
DB 63 AFGTIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITHTKEYAAAQVIERLSS 121

RESULT 3
AAM52130
ID AAM52130 standard; protein; 121 AA.
XX
AC AAM52130;
XX
DT 01-FEB-2002 (first entry)
XX
DE Bacillus subtilis ACPS.

XX Bacillus subtilis; ACPS; acyl carrier protein synthase; active site;
KW protein coordinate data; CoA binding site; X-ray crystallography;
KW Swiss Protein P96618.

XX Bacillus subtilis.
XX
FN WO200155340-A2.
XX
PD 02-AUG-2001.
XX
DE 26-JAN-2001; 2001WO-US002732.

XX 28-JAN-2000; 2000US-0178639P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PA (MILL-) MILLENNIUM PHARM INC.

XX Pariss KD, Somers WS, Tam AS, Lin LL, Stahl ML;
XX
XX WPI; 2001-476201/51.

PT Novel crystallized acyl carrier protein synthase enzyme used to identify
PT an activator or inhibitor of a molecule or complex comprising a CoA
PT binding site, and to determine the molecular structure of a molecule or
PT complex.

XX Disclosure; Fig 8; 181pp; English.

PS The invention relates to a crystallized acyl carrier protein synthase
CC (ACPS) enzyme used to identify an agent that interacts with the active
CC site, to identify an activator or inhibitor of a molecule or molecular
CC complex comprising a CoA binding site and to determine the molecular
CC structure. The present sequence is that of the Bacillus subtilis ACPS
XX

XX Sequence 121 AA;

Query Match 99.3%; Score 591; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 61
DB 3 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 62
QY 62 AFGTIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITHTKEYAAAQVIERLSS 120
DB 63 AFGTIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITHTKEYAAAQVIERLSS 121

RESULT 4
ABU18305
ID ABU18305 standard; protein; 119 AA.
XX

AC ABU18305;
 XX 19-JUN-2003 (first entry)
 DT
 DE Protein encoded by Prokaryotic essential gene #3832.
 XX
 KM Antisense, prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Bacillus anthracis.
 XX
 PN WO20027183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 XX
 PR 06-SEP-2001; 2001US-00948993.
 XX
 PR 25-OCT-2001; 2001US-0342823P.
 XX
 PR 08-FEB-2002; 2002US-00072851.
 XX
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KU, Zyckind JW;
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
 PI
 DR WPI; 2003-029926/02.
 DR N-Psdb; ACA22175.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 46229; 1766bp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation and the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 119 AA;
 SQ

Query Match 51.1%; Score 304; DB 6; Length 119;
 Best Local Similarity 54.2%; Prod. No. 2.5e-28;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

OY 3 GIGDITELKRIASWAGROKRFARILTRSELDQYELSEKRNKEFLAGFAEAFSKA 62
 |||||
 DB 4 GIGDITELKRIEKMLOGKLFMERILITENRANVAKLKGSRLLTEFVAGRRPAEAVSKA 63
 |||||
 OY 63 FGATGROLSPDIEIRKDNQKXPYIICTKLQAHVSVITHTVEYAAQVIERLSS 120
 |||||
 DB 64 VGTGKGVSLDIEVRNDRGKPIILTS--TEHIVHLSISHSKEFAVAQVLESSSS 119
 |||||

RESULT 5
 ABB47581
 ID ABB47581 standard; protein; 118 AA.
 XX
 AC ABB47581;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #285.
 XX
 KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KM vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 PN WO200177335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-FR001118.
 XX
 PR 11-APR-2000; 2000FR-00004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangoul L, Couve E, Rusanick C, Fslhi H, Dehoux P;
 PI Dusurget O, Chetouni F, Nedjari H, Glaser P, Kunst F, Coessart P;
 PI Daniels U, Goebel W, Krefft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Doman E, Hain T, Berche P, Chardic A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madeno E, De Pablos B, Weiland J, Kaerst U, Entian K, Haut J;
 PI Rose M, Voss H;
 XX
 DR WPI; 2002-010914/01.
 XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and related
 PT polypeptides.
 XX
 PS Claim 6; SEQ ID NO 286; 192pp; French.
 XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in *L.*
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of *L. monocytogenes* and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccines compositions for the treatment or prevention of infections by *L.*
 CC monocytogenes and related organisms. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 118 AA;
 SQ

CC		strains; or (13) identifying the target of a compound that inhibits the
CC		proliferation of an organism. The antisense nucleic acids are useful for
CC		identifying proteins or screening for homologous nucleic acids required
CC		for cellular proliferation to isolate candidate molecules for rational
CC		drug discovery programs, or for screening homologous nucleic acids
CC		required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,
CC		<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of
CC		the target prokaryotic essential genes. Note: The sequence data for this
CC		patent did not form part of the printed specification, but was obtained
CC		in electronic format directly from WIPO at
CC		ftp.wipo.int/pub/published_pct_sequences
XX		
SO	Sequence 118 AA;	
	Query Match	48.2%; Score 287; DB 6; Length 118;
	Best Local Similarity	50.9%; Pred. No. 2.8e-26;
	Matches	58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
OY		
D6		
	3 GIGDITELKRIAMAGROKQFAFRILTRTBEDLQGYVLSKRNEPLAFGRFAKAESKA 62	
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
	4 GIGIDMDLDLEKVQVEKNRPFIERVLTEKEIKOFEXEYEGNRKIETLAGRFKAKEYAKA 63	
OY		
	63 FGTGIGRSLOPDIERKDNGKPXYICTLGSQAAYVSITTHKEVAAAQVVIE 116	
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
D6		
	64 NGTGFGLHSLFTVDVELQVEDGRPHVTLPVKSGSENVSVITHRAKSAAQVIIE 117	
RESULT 7		
ABP39429	ID ABP39429 standard; protein: 124 AA.	
AC	ABP39429;	
XX		
DT	24-JUL-2002 (first entry)	
XX		
DE	Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4274.	
XX		
KW	Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;	
XX	antibacterial; gene therapy.	
OS	Staphylococcus epidermidis.	
XX		
PN	US6380370-B1.	
PD	30-APR-2002.	
XX		
PE	13-AUG-1998; 98US-00134001.	
PR	14-AUG-1997; 97US-0055779P.	
PR	08-NOV-1997; 97US-0064964P.	
XX		
PA	(GENO-) GENOME THERAPEUTICS CORP.	
PI	Doucette-Stamm LA, Bush D;	
DR	WP1; 2002-381255/41.	
DR	N-PSDB; ABN91974.	
XX		
PT	Novel isolated nucleic acid encoding a Staphylococcus epidermis	
PT	polypeptide, useful for diagnosing and treating bacterial infections.	
XX		
PS	Disclosure; SEQ ID NO 4274; 267pp; English.	
XX		
CC	ABN90558 to ABN93374 represent Staphylococcus epidermidis open reading	
CC	frame (ORF) nucleic acid sequences which encode the amino acid sequences	
CC	given in ABP35124 to ABP37960. The <i>S. epidermidis</i> sequences have	
CC	antibacterial activity and can be used in gene therapy. The sequences can	
CC	also be used in the diagnosis and treatment of bacterial infections,	
CC	particularly <i>S. epidermidis</i> infections. The sequences can be used to	
CC	screen for compounds able to interfere with the <i>S. epidermidis</i> life cycle	
CC	or inhibit <i>S. epidermidis</i> infection. N.B. The sequence data for this	
CC	patent did not form part of the printed specification, but was obtained	
CC	in electronic format directly from the USPRO web site	

XX Sequence 124 AA;
SQ

Query Match 47.3%; Score 281.5; DB 5; Length 124;
Best Local Similarity 51.3%; Pred. No. 1.4e-25;
Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;

2 YGIGDITELKRIASMAQRKFAERILT--RSELDQYELSEKRNKFLAGRPAAKEA 58
10 YGIGDILIEIRIKMLQ-NQTKFIERILTEERDKLNQY--TNEQRRLFEFLAGRPVXEA 66

59 FSKAGTGTGIRQLSFQDIEIRKQNGKPYITCTKLSQAAVHVSITHTKEVAAOVVIER 117
67 FSKALGTGIGKSVSFQDINCYNDAIGKP---CIDYPGFYTHVSIHTENYAMSOVITLTK 122

RESULT 8
ADS04560 standard; protein, 124 AA.
ADS04560;
ADS04560;
04-NOV-2004 (first entry)

Staphylococcus epidermis polypeptide seqid 3855.
antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
recombinant expression vector; infection; computer readable medium;
computer based system.
Staphylococcus epidermidis.
US2004147734-A1.
29-JUL-2004.
01-DEC-2003; 2003US-00724972.
08-NOV-1997; 97US-0064964P.
13-AUG-1998; 98US-00134001.
29-NOV-1999; 99US-00450969.
(DOUC/) DOUCETTE-STAMM L.
(BUSH/) BUSH D.
Doucette-Stamm L, Bush D;
WPI; 2004-580138/56.
N-PSDB; ADS00788.

New isolated polypeptide and encoding nucleic acid derived from
Staphylococcus epidermidis, useful for diagnosing, preventing and/or
treating an S. epidermidis bacterial infection.
Claim 17; SEQ ID NO 3855; 741bp; English.

The invention describes an isolated nucleic acid comprising a nucleotide
sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
given in the specification. Also described are: a recombinant expression
vector; a cell comprising a recombinant expression vector of (1);
a producing an S. epidermidis polypeptide; an isolated nucleic acid
comprising a nucleotide sequence of at least 8 nucleotides in length; a
vaccine composition for prevention or treatment of an S. epidermidis
infection, comprising a nucleic acid cited above and a carrier; treating
a subject for S. epidermidis infection; a recombinant or substantially
pure preparation of an S. epidermidis polypeptide or its fragment; a
vaccine composition for prevention or treatment of an S. epidermidis
infection; detecting the presence of a Staphylococcus nucleic acid in a
sample; a computer readable medium having recorded in it the nucleotide
sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
system for identifying fragments of the Staphylococcus genome of

CC commercial importance; a computer based system for identifying fragments
CC of the Staphylococcus plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the Staphylococcus
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the Staphylococcus genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an Staphylococcus epidermidis bacterial
CC infection. This is the amino acid sequence of a S. epidermis protein of
CC the invention.
CC
XX
XX

Sequence 124 AA;
SQ

Query Match 47.3%; Score 281.5; DB 8; Length 124;
Best Local Similarity 51.3%; Pred. No. 1.4e-25;
Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;

2 YGIGDITELKRIASMAQRKFAERILT--RSELDQYELSEKRNKFLAGRPAAKEA 58
10 YGIGDILIEIRIKMLQ-NQTKFIERILTEERDKLNQY--TNEQRRLFEFLAGRPVXEA 66

59 FSKAGTGTGIRQLSFQDIEIRKQNGKPYITCTKLSQAAVHVSITHTKEVAAOVVIER 117
67 FSKALGTGIGKSVSFQDINCYNDAIGKP---CIDYPGFYTHVSIHTENYAMSOVITLTK 122

RESULT 9
ABU42933 standard; protein, 117 AA.
ABU42933;
ABU42933;
19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #28460.
Antisense; prokaryotic essential gene; cell proliferation; drug design.
Staphylococcus epidermidis.
WO200271183-A2.
03-OCT-2002.
21-MAR-2002; 2002WO-US009107.
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
(ELIT-) ELITRA PHARM INC.
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW,
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
WPI; 2003-029926/02.
N-PSDB; ACA46803.

New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular functions or to
PT isolate candidate molecules for rational drug discovery programs.
Claim 25; SEQ ID NO 70857; 1766bp; English.

The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC the gene product or that has an activity against a biological pathway
 CC identifying a gene required for cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

CC Sequence 117 AA;
 SQ
 Query Match 47.0%; Score 279.5; DB 6; Length 117;
 Best Local Similarity 51.3%; Pred. No. 2.2e-25;
 Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;
 QY 2 YGIGDITELKRIASMAQRKRPFAERILT--RSELDQYVELSEKRNKFLGRPAKKA 58
 DB 3 YGIGDLEIRIKAKAFKQKDKVKRLTBEEDQPHFSSEKRNKFLGRPAKKA 59
 QY 59 SKAFGTGIGRQLSFODIIRKQNGKPYITCTKLSQAAVHSITHTKEAQAQVIER 117
 DB 60 FSKALGTGIGKSVSFODINCYNDAIGKP---CIDYPGFYTHVSIHTENYAMSQVILEK 115

RESULT 10
 ABU43645
 ID ABU43645 standard; protein; 119 AA.
 AC ABU43645;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by prokaryotic essential gene #29172.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Staphylococcus haemolyticus*.
 XX
 PN WO200271183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 XX
 PR 06-SEP-2001; 2001US-00948993.
 XX
 PR 25-OCT-2001; 2001US-0342923P.
 XX
 PR 08-FEB-2002; 2002US-00072851.
 XX
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-1) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zvekind JW,
 XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR WPI; 2003-029926/02.
 XX N-PSDB; ACA47515.
 XX

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS Claim 25; SEQ ID NO 71569; 1766p; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 XX the 6213 antisense sequences given in the specification where expression
 XX of the nucleic acid inhibits proliferation of a cell. Also included are:
 XX (1) a vector comprising a promoter operably linked to the nucleic acid
 XX encoding a polypeptide whose expression is inhibited by the antisense
 XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
 XX polypeptide or its fragment whose expression is inhibited by the
 XX antisense nucleic acid; (4) an antibody capable of specifically binding
 XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 XX proliferation or the activity of a gene in an operon required for
 XX proliferation; (7) identifying a compound that influences the activity of
 XX the gene product or that has an activity against a biological pathway
 XX required for proliferation, or that inhibits cellular proliferation; (8)
 XX identifying a gene required for cellular proliferation or the biological
 XX pathway in which a proliferation-regulated gene or its gene product lies
 XX or a gene on which the test compound that inhibits proliferation of an
 XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
 XX compound's activity; (11) a culture comprising strains in which the gene
 XX product is overexpressed or underexpressed; (12) determining the extent
 XX to which each of the strains is present in a culture or collection of
 XX strains; or (13) identifying the target of a compound that inhibits the
 XX proliferation of an organism. The antisense nucleic acids are useful for
 XX identifying proteins or screening for homologous nucleic acids required
 XX for cellular proliferation to isolate candidate molecules for rational
 XX drug discovery programs, or for screening homologous nucleic acids
 XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 XX the target prokaryotic essential genes. Note: The sequence data for this
 XX patent did not form part of the printed specification, but was obtained
 XX in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

Sequence 119 AA;

Query Match 46.8%; Score 278.5; DB 6; Length 119;
 Best Local Similarity 50.0%; Pred. No. 3e-25;
 Matches 59; Conservative 22; Mismatches 32; Indels 5; Gaps 3;
 QY 2 YGIGDITELKRIASMAQRK-RFAERILITSELDQYVEL-SEKRNKFLGRPAKKA 59
 DB 3 YGIGDLEIRIKAKAFKQKDKVKRLTBEEDQPHFSSEKRNKFLGRPAKKA 62
 QY 60 SKAFGTGIGRQLSFODIIRKQNGKPYITCTKLSQAAVHSITHTKEAQAQVIER 117
 DB 63 SKALGTGIGKTVAFDINCYNDAIGKP---CIDYNGFYTHVSIHTENYAMSQVILEK 117

RESULT 11
 ABR83238
 ID ABR83238 standard; protein; 119 AA.
 AC ABR83238;
 XX
 DT 30-SEP-2003 (first entry)
 XX
 DE *S. aureus* acyl carrier protein synthase acps protein SEQ ID NO:32.
 XX
 KW Crystallised recombinant polypeptide; *Staphylococcus aureus*; vaccine;
 KW *Streptococcus pneumoniae*; Helicobacter pylori; *Pseudomonas aeruginosa*;
 KW membrane biosynthesis; crystal form; antibacterial; crystal structure;
 KW immunological response; vaccination; fte2; fab2; fabd; acps; murD; murC;
 KW fabH; tagd; obg.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN WO2003027139-A2.
 XX

XX	03-APR-2003.
PD	24-SEP-2002; 2002MO-CA001443.
XX	24-SEP-2001; 2001US-0324449P.
XX	24-SEP-2001; 2001US-0324504P.
PR	01-OCT-2001; 2001US-0326269P.
PR	03-OCT-2001; 2001US-0336887P.
PR	24-OCT-2001; 2001US-0339560P.
PR	25-OCT-2001; 2001US-0337471P.
PR	26-OCT-2001; 2001US-0340002P.
PR	26-OCT-2001; 2001US-0340027P.
PR	18-DEC-2001; 2001US-0341767P.
PR	21-DEC-2001; 2001US-0344307P.
PR	27-DEC-2001; 2001US-0345946P.
PA	(AFPI-) AFFINUM PHARM INC.
PI	Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
PI	Canadenn V, Domagala W, Houston S, Kanagarajah D, Li Q, Mansoury K;
PI	McDonald M, Neckov S, Ng I, Pander B, Sheldrick B, Vallee F;
PI	Viola C, Wrezel O;
DR	WPI; 2003-441048/41.
XX	N-PSDB; ACP06197.
XX	Novel crystallized recombinant polypeptides from <i>Staphylococcus aureus</i> ,
PT	<i>Streptococcus pneumoniae</i> and <i>Helicobacter pylori</i> and which are involved
PT	in membrane biosynthesis, useful as targets for pathogenic bacteria.
XX	Claim 84; Fig 27; 312pp; English.
XX	The present invention describes a crystallised recombinant polypeptide
CC	(I) comprising amino acid sequence of polypeptides from <i>Staphylococcus</i>
CC	<i>aureus</i> , <i>Streptococcus pneumoniae</i> , <i>Helicobacter pylori</i> and <i>Pseudomonas</i>
CC	<i>aeruginosa</i> and which are involved in membrane biosynthesis, or amino acid
CC	sequences having at least 90 % identity with the polypeptide sequence,
CC	where the polypeptide is in crystal form. (1) has antibacterial activity
CC	and can be used in vaccines. (1) is useful for designing a modulator for
CC	the prevention or treatment of <i>S. aureus</i> , <i>H. pylori</i> , <i>S. pneumoniae</i> , and
CC	<i>P. aeruginosa</i> -related disease or disorder. (1) is also useful for
CC	identifying small molecules that bind to a recombinant polypeptide. The
CC	structural and functional information of (1) aid in the discovery and
CC	design of therapeutic and diagnostic molecules. The crystal structure is
CC	useful to make a structural or computer model of the polypeptide, complex
CC	or its portion. (1) can be used for inducing an immunological response in
CC	an individual and as an antigen for vaccination of a host to produce
CC	specific antibodies which protect against invasion of bacteria, for
CC	example by blocking adherence of bacteria to damaged tissue. ACP06185 to
CC	ACF06232 and ABR83203 to ABR83333 represent sequences used in the
XX	exemplification of the present invention
XX	Sequence 119 AA:
QY	Query Match 46.7%; Score 278; DB 6; Length 119;
Db	Best Local Similarity 48.7%; Pred. No. 3, 5e-25;
Matches	57; Conservative 25; Mismatches 31; Indels 4; Gaps 2
QY	2 YGIGDLITLKRYSAGROKRAEILIRSELDQYELS-EKKNEFLAGRPAAKEARS 60
Db	3 HGIQGLDILIDIRQAAYSROPKLVETILTKNEGHKNNFTHEORKLEPLAAGRATVEARS 62
QY	61 KAFGTGIGRGLSFODIEIRDOQNGKRYIICTKLSQAAYVSIHTFTREYAAQVIER 117
Db	63 KALGTGIGKRVAPNDIDCYNDELGRKFI--DYEGFTIVHSISHTHYAMSQVYVLEK 116
RESULT 12	
ID	ABM71799 standard; protein; 119 AA.
AC	ABM71799.

XX	20-NOV-2003	(first entry)
DT	Staphylococcus aureus protein #1039.	
XX		
DE	Staphylococcus aureus protein #1039.	
XX	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;	
KW	enzymatic assay; antibiotic target.	
XX		
OS	Staphylococcus aureus.	
XX		
PN	MO200294868-A2.	
PD		
XX	28-NOV-2002.	
PF	27-MAR-2002; 2002MO-IB002637.	
XX		
PR	27-MAR-2001; 2001GB-00007661.	
XX		
PA	(CHIR-) CHIRON SPA.	
XX		
PI	Maignani V, Mora M, Scarselli M;	
XX		
DR	WPI; 2003-120786/11.	
XX		
DR	N-PSDB; ACF73359.	
XX		
PT	New Staphylococcus aureus protein, useful as a vaccine for treating or	
XX	preventing Staphylococcal infection, specifically an infection caused by	
PT	S. aureus, e.g. sepsis.	
XX		
PS	Claim 1; SEQ ID NO 2078; 49pp; English.	
XX		
CC	The invention relates to novel genes and encoded proteins from	
XX	Staphylococcus aureus. A composition comprising the S. aureus protein, a	
CC	nucleic acid encoding the protein, or an antibody to the protein, is	
XX	useful as a pharmaceutical, particularly as a vaccine for treating or	
CC	preventing infection due to Staphylococcus bacteria, specifically an	
CC	infection caused by S. aureus. The composition is particularly useful for	
XX	treating or preventing sepsis in a patient. The composition can also be	
CC	used for diagnostics. The protein is also used in an assay for enzymatic	
CC	studies and as a target for antibiotics. This sequence represents one of	
CC	the novel S. aureus proteins of the invention	
XX		
SEQ	Sequence 119 AA;	
XX		
Query Match	46.7%; Score 278; DB 6; Length 119;	
Best Local Similarity	48.7%; Pred. 3.5e-25;	
Matches	57; Conservative 25; Mismatches 31; Indels 4; Gaps 2	
QY	2 YGIGDIDIEIKRIASMAGRQKRFARITRSELDQYEIS-EKRKNEFLAGRFPAKAPFS 60	
DB	3 HGIQDLLEIDRIQLMYSKQPLVBRILTKNQHGFNNFTTHQRIEFLAGRFATKEAFS 62	
QY	61 KAFGTGIGRQLSFQDIEIRKQNGKRPYIITCKLSQAAVHSITHTKEVAAQVIER 117	
DB	63 KALGTGLGHNVAFNIDICYNDELGRPKI---DYEGFIVHSISHTEHYMSQVLEK 116	
RESULT 13		
AAU33845		
ID	AAU33845 standard; protein; 119 AA.	
AC	AAU33845;	
XX		
DT	14-FEB-2002 (first entry)	
XX		
DE	Staphylococcus aureus cellular proliferation protein #121.	
XX		
KW	Antisense; prokaryotic cellular proliferation protein; antibiotic;	
XX	antibacterial; drug design.	
XX		
OS	Staphylococcus aureus.	
XX		
EN	MO200170955-A2.	

```
XX XX      27-SEP--2001.
PD PD
PF PF      21-MAR--2001;   2001WO-US0009180.
XX XX
PR PR      21-MAR--2000;   2000US-01901078P.
PR PR      23-MAY--2000;   2000US-0206848P.
PR PR      26-MAY--2000;   2000US-0207727P.
PR PR      23-OCT--2000;   2000US-0242578P.
PR PR      27-NOV--2000;   2000US-0253625P.
PR PR      22-DEC--2000;   2000US-0257931P.
PR PR      16-FEB--2001;    2001US-0269308P.
XX XX
PA PA      (ELIT-) ELITRA PHARM INC.
XX XX
PI PI      Haeselbeck R, Ohlssen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
PI PI      Yamamoto RT, Xu HH;
DR DR      WPI, 2001-611495/70.
XX XX      N-PADB; AABS1704.
PT PT
PT PT      New polynucleotides for the identification and development of
PS PS      antibiotics, comprise sequences of antisense nucleic acids.
XX XX      Example 3; SEQ ID NO 5341; 511pp; English.
CC CC      The invention relates to antisense inhibitors of genes essential to
CC CC      prokaryotic cellular proliferation, their use in identifying the genes,
CC CC      their use in the discovery of novel antibiotics, the essential genes
CC CC      themselves and the encoded proteins. The prokaryotes used are Escherichia
CC CC      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC CC      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC CC      useful for the identification of potential new targets for antibiotic
CC CC      development. The antisense nucleic acids can also be used to identify
CC CC      proteins used in proliferation, to express these proteins, and to obtain
CC CC      antibodies capable of binding to the expressed proteins. The proteins can
CC CC      be used to screen compounds in rational drug discovery programmes. The
CC CC      antisense nucleic acid sequence is also useful to screen for homologous
CC CC      nucleic acids which are required for cell proliferation in a wide variety
CC CC      of organisms. The present sequence represents an essential prokaryotic
CC CC      cellular proliferation protein. Note: The sequence data for this patent
CC CC      did not form part of the printed specification, but was obtained in
CC CC      electronic format directly from WIPO at
CC CC      ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ SQ      Sequence 119 AA;

Query Match          46.6%; Score 277; DB 4; Length 119;
Best Local Similarity 48.7%; Pred: No. 4,6e-25;
Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2

QY        2 YGIGDITELEKTIASWAGROKRFAERILTRSELDQYYELS-EKKRNEFLAGRPAAKEAFS 60
DYB       3 HGIQGVDLIRIDRIKVLYSKOPKLVERILTLPKNQHKKNNFTTBQRKTIEFLAQPATYEARS 62

QY         61 KAPFGICIGQLSFODIETFRKDQNGRKRYIICTKLQAAVHVSITHTEKYAAPVVIER 117
DB         63 KALGTGLGGHAVFNDICYNDELGRPKI--DYEGFIVHSVISHTEQYAMQSOWLEIK 116

RESULT 14
ID AUU36808 standard, protein; 119 AA.
AC AUU36808;
DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #978.
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
```

[illegible]

KW Acps; phosphopantetheinyl transferase; antibacterial;
KW Helicobacter pylori; stomach cancer; ulcer; gastritis.
XX
OS Staphylococcus aureus.

XX WO200040594-A1.

XX 13-JUL-2000.

XX 13-DEC-1999; 99WO-US029464.

XX 08-JAN-1999; 99US-00227700.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Pearson SC;

XX WPI; 2000-465946/40.

DR N-PSDB; AAA73679.

XX New isolated Staphylococcus aureus polypeptide, referred to as Acps, for
PT treating or diagnosing individuals with a disease in need of enhanced or
PT inhibited activity or expression of the polypeptide.

XX Claim 1; Page 3; 38pp; English.

XX The present sequence is the Staphylococcus aureus phosphopantetheinyl
CC transferase family protein Acps. The DNA encoding this sequence was
CC isolated from a Staphylococcus aureus DNA library. The Acps protein and
CC its agonists, antagonists or nucleic acids may be used to treat
CC individuals that are in need of enhanced or inhibited activity or
CC expression of the protein, or an immunological response to it. They may
CC also be used to detect and treat microbial diseases, such as Helicobacter
XX pylori infections that cause stomach cancer, ulcers and gastritis

XX Sequence 119 AA;

Query Match 46.2%; Score 275; DB 3; Length 119;

Best Local Similarity 48.7%; Pred. No. 8e-25; Matches 57; Conservative 24; Mismatches 32; Indels 4; Gaps 2;

OY 2 YGIGDITELKRIASAGQKRPARIITRSELDQYELS-EKKKEFIAGRFPAKEAFS 60
DB 3 HGIQVDLIRIDIRIKVLSKOPKXVERILTKNEQHKFNFTBQRKIEFLAGRFATKEAFS 62
OY 61 KAFGIGIGRQLSPQDIIRKQNGKPYICTKLSQAQVHSITHTKEVAAQVIER 117
DB 63 KALGTGLGKHAANDIDICYNDELGRPKI--DYEGFIVHSISHTHTYAMSQVVLK 116

Search completed: December 21, 2005, 13:49:13
Job time : 161.806 secs

This Page Blank (uspto)

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:54:50 ; Search time 5.64179 Seconds
(without alignments)
102.397 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397
Sequence: 1 GIGSGADTLERVTIKTIIVDL.....EDAEKIAIVGDAVNYIQNOQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB pep:*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB pep:*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB pep:*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB pep:*
6: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB pep:*
7: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	54.7	76	US-10-467-657-4016	Sequence 4016, App
2	217	54.7	78	US-10-467-657-3996	Sequence 3996, App
3	217	54.7	78	US-10-467-657-7044	Sequence 7044, App
4	135	34.0	178	US-10-821-234-1052	Sequence 1052, App
5	94.5	23.8	2910	US-11-087-100-2	Sequence 2, Appl1
6	94.5	23.8	2910	US-11-087-084-2	Sequence 2, Appl1
7	94.5	23.8	2910	US-11-087-085-2	Sequence 2, Appl1
8	91.5	23.0	86	US-11-087-100-13	Sequence 13, Appl1
9	91.5	23.0	86	US-11-087-084-13	Sequence 13, Appl1
10	91.5	23.0	86	US-11-087-085-13	Sequence 13, Appl1
11	73.5	18.5	321	US-10-467-9628-41	Sequence 41, Appl1
12	68	17.1	697	US-11-074-176-214	Sequence 214, App
13	65.5	16.5	412	US-11-082-389-96	Sequence 96, Appl1
14	62.5	15.7	642	US-10-467-657-5900	Sequence 5900, App
15	62.5	15.5	1061	US-11-059-814-18	Sequence 18, Appl1
16	61.5	15.5	530	US-10-858-730-67	Sequence 67, Appl1
17	61	15.4	1001	US-10-467-9628-81	Sequence 81, Appl1
18	60	15.1	327	US-11-129-143-91	Sequence 91, Appl1
19	60	15.1	1766	US-11-075-185-10	Sequence 10, Appl1
20	59.5	15.0	188	US-11-194-246-292	Sequence 232, App
21	59	14.9	122	US-10-793-626-564	Sequence 564, App
22	59	14.9	128	US-11-105-864-4	Sequence 4, Appl1
23	59	14.9	274	US-10-467-657-2140	Sequence 2140, App
24	59	14.9	449	US-10-485-517-272	Sequence 272, App
25	58.5	14.7	269	US-10-793-626-2472	Sequence 2472, App

26	58.5	14.7	345	6	US-10-485-517-314	Sequence 314, App
27	58.5	14.7	353	7	US-10-793-626-2730	Sequence 2730, App
28	58.5	14.7	431	7	US-11-060-920-4	Sequence 4, Appl1
29	58.5	14.7	872	7	US-11-077-550-145	Sequence 145, App
30	58.5	14.7	879	7	US-11-077-550-143	Sequence 143, App
31	58.5	14.7	887	7	US-11-077-550-147	Sequence 147, App
32	58.5	14.7	1315	7	US-11-077-550-141	Sequence 141, App
33	58	14.6	424	6	US-10-793-626-2296	Sequence 2296, App
34	58	14.6	484	6	US-10-467-657-6816	Sequence 6816, App
35	58	14.6	1196	6	US-10-613-744-9	Sequence 9, Appl1
36	57.5	14.5	597	6	US-10-467-657-3020	Sequence 3020, App
37	57.5	14.5	610	6	US-10-858-730-292	Sequence 292, App
38	57.5	14.5	720	6	US-10-793-626-2058	Sequence 2058, App
39	57.5	14.5	1804	6	US-10-513-786-2	Sequence 2, Appl1
40	57.5	14.5	3704	6	US-10-821-234-1573	Sequence 1, Appl1
41	57	14.4	635	6	US-10-821-234-1573	Sequence 1573, App
42	57	14.4	724	6	US-10-821-234-1506	Sequence 1506, App
43	57	14.4	1163	7	US-11-044-899-2	Sequence 2, Appl1
44	57	14.4	1163	7	US-11-044-899-30	Sequence 30, Appl1
45	56.5	14.2	341	6	US-10-793-626-1278	Sequence 1278, App

ALIGNMENTS

```
RESULT 1
US-10-467-657-4016
; Sequence 4016, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4016
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4016

Query Match      54.7%; Score 217; DB 6; Length 76;
Best Local Similarity 66.2%; Pred. No. 9.1e-16;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Cy      10 ERYTKTIIVRLGVADVADKLEAFKEDLGADSLDVELVMELEDFDEPDEISDEDAEKIAT 69
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      4 QGVKKIIAQLGNEADVKNESFFQDDLGADSLDVELVMALEAARGCEIPEDAKITT 63

Cy      70 VGDVAVNYI 77
      |::|::|
Db      64 VGLAIDYI 71

RESULT 2
US-10-467-657-3996
; Sequence 3996, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

```
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3996
LENGTH: 78
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3996

Query Match
Best Local Similarity 54.7%; Score 217; DB 6; Length 78;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Db
10 EBYTKIIVRLGVDEADVLEASFKEKDLGADSLDVVELVMELEDEPFDEMEISDEDAEKIAT 69
6 QGVKIIAEQLGVNEADVKNESFFQDGLGADSLDVVELVMALEBAFGCEIPDEDAEKITT 65

QY
70 VGDVAVNYI 77
66 VOLAIDYI 73

Db
66 VOLAIDYI 73

RESULT 3
US-10-467-657-7044
Sequence 7044, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIANNI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7044
LENGTH: 78
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7044

Query Match
Best Local Similarity 54.7%; Score 217; DB 6; Length 78;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Db
10 EBYTKIIVRLGVDEADVLEASFKEKDLGADSLDVVELVMELEDEPFDEMEISDEDAEKIAT 69
6 QGVKIIAEQLGVNEADVKNESFFQDGLGADSLDVVELVMALEBAFGCEIPDEDAEKITT 65

QY
70 VGDVAVNYI 77
66 VOLAIDYI 73

Db
66 VOLAIDYI 73

RESULT 4
US-10-821-234-1052
Sequence 1052, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
```

```
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 1052
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1052

Query Match
Best Local Similarity 34.0%; Score 135; DB 6; Length 178;
Matches 30; Conservative 17; Mismatches 33; Indels 0; Gaps 0;

Db
2 PLGSADTLERYTKIIVRLGVDEADVLEASFKEKDLGADSLDVVELVMELEDEPFDEMEISD 61
95 PLTEGIODRVLVLYKLYDKIDPEKLSVSHFMKDLGSLDVQVEIIMAMDEDFGEIIPD 154

QY
62 EDAEKIATVGDVAVNYIONQ 81
155 IDAEKLMCPQGEIVDYIDKK 174

Db
155 IDAEKLMCPQGEIVDYIDKK 174

RESULT 5
US-11-087-100-2
Sequence 2, Application US/11087100
Publication No. US20050266440A1
GENERAL INFORMATION:
APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Platt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORF of a PUFA Polyketide Synthase
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087,100
CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 2910
TYPE: PRT
ORGANISM: Schizochytrium sp.
US-11-087-100-2

Query Match
Best Local Similarity 23.8%; Score 94.5; DB 7; Length 2910;
Matches 26; Conservative 18; Mismatches 26; Indels 13; Gaps 3;

Db
2 PLGSADTLERYTKIIVRLGVDEADVLEASFKEKDLGADSLDVVELVMELEDEPFDEMEISD 53
1114 PAVSNELEKAEYVMEVLAKTGYETDMTEADMELET---ELGIDSIKVEIISVQ 1169

QY
54 EFDMEISDEDA-EKIATVGDVAVN 75
1170 MLNVEAKVDALSRRTVGEVNV 1192

Db
1170 MLNVEAKVDALSRRTVGEVNV 1192

RESULT 6
US-11-087-084-2
Sequence 2, Application US/11087084
Publication No. US20050273883A1
```

Query Match	23.8%	Score 94.5	DB 7	Length 2910	
Best Local Similarity	31.3%	Pred. No. 0.12			
Matches	26	Conservative 18	Mismatches 26	Indels 13	
				Gaps 3	
QY	2	PLGSAADLTERTKIIVDLRLGVD	----	-ADVYKLEAFKEDGADSLDVLVWLELED	53
Db	1114	PAVSNELLLEKAKETVMEVTLAKGTGYETDMEIADMELET	----	ELGIDISIKRVELLSEVOA	1169
QY	54	EFDMIEISDEDA-EKIKATVGDAVN	75		
		:::			
Db	1170	MLNVEAKVDVALSRRTVGEAVN	1192		

Query Match	23.8%	Score	94.5	DB	7	Length	2910
Best Local Similarity	31.3%	Pred.	No. 0.12				
Matches	26	Conservative	18	Mismatches	26	Indels	13
						Gaps	3

```
Query Match      23.0%; Score 91.5; DB 7; Length 86;  
Best Local Similarity   31.2%; Pred.No. 0.0033;  
Matches    25; Conservative     18; Mismatches    24; Indels       13; Gaps        3;
```

```
Oy          5 SADTLERTKTIIVRLGVD-----EADVKLEASFKEPDIGADSLDVVELVMELDEDFD 56  
           | : || : ||| :  
Db          3 SNEILFKETIYVMEVLAKTGYETDMIEADMELFT----BLGDISIKRVEILTSEVGMLN 58
```

```
Oy          57 MEISDED-EKIATVGDVN 75  
           |:||::|:||:  
Db         59 VEAKDVDAISRRTTVGEVVN 78
```

```
RESULT 9  
US-11-087-084 -13  
 ; Sequence 13, Application US/11087084  
 ; Publication No. US2005027383A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Metz, James  
 ; APPLICANT: Barclay, William  
 ; APPLICANT: Flatt, James  
 ; APPLICANT: Kumer, Jerry  
 ; TITLE OF INVENTION: Nucleic Acid Molecular Encoding ORFA of a PUFA Polyketide Synthas  
 ; TITLE OF INVENTION: System and Uses thereof  
 ; FILE REFERENCE: 2997-29  
 ; CURRENT APPLICATION NUMBER: US/11/087, 084  
 ; CURRENT FILING DATE: 2005-03-21  
 ; PRIOR APPLICATION NUMBER: 09/231, 899  
 ; PRIOR FILING DATE: 1999-01-14  
 ; PRIOR APPLICATION NUMBER: 60/284, 066  
 ; PRIOR FILING DATE: 2001-04-16  
 ; PRIOR APPLICATION NUMBER: 60/298, 796  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/323, 269
```

```

; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Schizochytrium sp.
US-11-087-084-13

Query Match      23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033;
Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;

QY 5 SADTLERVTIKIIVDLGVD-----EADVKLEASFKEKEDLGADSLDVEIVLMELEDED 56
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 3 SHELLEKETVMEVLAATGYETDMIEADMELET---ELGIDSIKRVETLISEVOAMLN 58
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 57 MEISDEDA-EKIAIVGDVAVN 75
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 59 VEAKVDALSRRTTGEVAVN 78

RESULT 10
US-11-087-085-13
; Sequence 13, Application US/11087085
; Publication No. US20050273884A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kumer, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; TITLE OF INVENTION: System and Uses Thereof
; FILE REFERENCE: 2997-23
; CURRENT APPLICATION NUMBER: US/11/087,085
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Schizochytrium sp.
US-11-087-085-13

Query Match      23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033;
Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;

QY 5 SADTLERVTIKIIVDLGVD-----EADVKLEASFKEKEDLGADSLDVEIVLMELEDED 56
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 3 SHELLEKETVMEVLAATGYETDMIEADMELET---ELGIDSIKRVETLISEVOAMLN 58
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 57 MEISDEDA-EKIAIVGDVAVN 75
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 59 VEAKVDALSRRTTGEVAVN 78

RESULT 11
US-10-467-962B-41
; Sequence 41, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
```

```

; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herpicide/Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-41

Query Match      18.5%; Score 73.5; DB 6; Length 371;
Best Local Similarity 26.8%; Pred. No. 1.2;
Matches 26; Conservative 19; Mismatches 33; Indels 19; Gaps 3;

QY 4 GSADTLERVTIKIIVDLGVDADVKLEASFKEKEDLGADSLDV-----VELV 48
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 274 GSDEIERLRKRFACIGLFGVVDLIDYTKSSKELGKTACKDLADKLTTPKIMGLEKS 333
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 49 MELEDEFPMEISDE---DAEKIAIVGDVAVNYIQNOQ 81
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 334 REPAEKLNRBARDDQLGFDSDKVAPLALANYIAYRQ 370

RESULT 12
US-11-074-176-214
; Sequence 214, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Kluenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-214

Query Match      17.1%; Score 68; DB 7; Length 697;
Best Local Similarity 27.6%; Pred. No. 9.2;
Matches 21; Conservative 14; Mismatches 27; Indels 14; Gaps 2;

QY 2 PLGSADTLERVTIKIIVDLGVDADVKLEASFKEKEDLGADSLDV-----VELV 53
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 167 PLGSADTFEGVADILINWADIIYDEBKGSKMDTVFPDVEYKEAEKRAALIEAVADV 226
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 54 EF-----DMEISDED 63
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 227 NIMEKYLGGERISNDE 242

RESULT 13
US-11-082-389-96
; Sequence 96, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
```

APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habehauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US/11/082,389
PRIOR FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931550.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932134.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
Remaining prior application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 96
LENGTH: 412
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-082-389-96

Query Match 16.5%; Score 65.5; DB 7; Length 412;
Best Local Similarity 30.3%; Pred. No. 8.6;
Matches 20; Conservative 8; Mismatches 19; Indels 19; Gaps 2;
QY 10 ERTKTIIVRLGVDEADVLEKLEASFKEDLGADSLDVEVLVMELEDFPMEISDDAEKAT 69
DB 242 ERYARVVAELGVDEVAELMP-----DKLEIVELQDQ-----GRVVM 282
QY 70 VGDVN 75
DB 283 VGDVN 288

RESULT 14
US-10-467-657-5900
Sequence 5900, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASNANI Vega
APPLICANT: MONACT Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 5900
LENGTH: 642
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5900

Query Match 15.7%; Score 62.5; DB 6; Length 642;
Best Local Similarity 27.7%; Pred. No. 29;
Matches 23; Conservative 11; Mismatches 46; Indels 3; Gaps 1;
QY 2 PLGSADTLERYTKIIVRLGVDEADVLEKLEASFKEDLGADSLDVEVLVMELEDFPME 58
DB 157 PGSIABILELLEIKCKDEIRDEVEVAIIDPREVLNLELGLHLETTAPEKPSNDSDEN 216
QY 59 ISDEDAEKIATVGDVNTIQNDQ 81
DB 217 EDDSESEBDADRIISANLAEKQ 239

RESULT 15
US-11-059-814-18
Sequence 18, Application US/11059814
Publication No. US20050272650A1
GENERAL INFORMATION:
APPLICANT: University of South Florida
APPLICANT: Monapetra, Shyam
TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
TITLE OF INVENTION: Proliferation Disorders
FILE REFERENCE: USF-215PTC2
CURRENT APPLICATION NUMBER: US/11/059,814
PRIOR FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: 60/521,072
PRIOR FILING DATE: 2004-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 1061
TYPE: PRT
ORGANISM: Homo sapiens
US-11-059-814-18

Query Match 15.6%; Score 62; DB 7; Length 1061;
Best Local Similarity 29.3%; Pred. No. 61;
Matches 22; Conservative 10; Mismatches 29; Indels 14; Gaps 2;
QY 1 GPLGSADTLERYTKIIVRLGVDEADVLEKLEASFKEDLGADS--LDVEVLVMELEDFPME 58
DB 864 GETVQAELAFDSVTIYPSDVGFTA-----LSAESTPMQVVTLLNDLXTCFNAV 911
QY 59 ISDEDAEKIATVGDGA 73
DB 912 IDNFVYKVEITIGDA 926

Search completed: December 21, 2005, 14:13:51
Job time : 6.64179 secs

This Page Blank (uspto)


```

; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
; FILE REFERENCE: 2368/14
; CURRENT FILING DATE: 2003-11-19
; PRIOR FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2000-05-08
; PRIOR FILING DATE: 2000-05-06
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-717-138-1

Query Match      100.0%; Score 397; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.7e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGSADTLERYTKIIVDRIGVDEADYKLEASFKEKDLGADSLDVVELVMELEDFPMETS 60
Db 1 GPLGSADTLERYTKIIVDRIGVDEADYKLEASFKEKDLGADSLDVVELVMELEDFPMETS 60

Qy 61 DEDAEXIATVGDVAVNYIQNQ 81
Db 61 DEDAEXIATVGDVAVNYIQNQ 81

RESULT 3
US-10-282-122A-46208
; Sequence 46208, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46208
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46208

Query Match      77.3%; Score 307; DB 4; Length 80;
Best Local Similarity 82.9%; Pred. No. 1.4e-25;
Matches 63; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GSADTLERYTKIIVDRIGVDEADYKLEASFKEKDLGADSLDVVELVMELEDFPMETS 63
Db 3 GMADVLERVTKIIVDRIGVDEADVPPASFKEDLGADSLDVVELVMELEDFPMETS 62

Qy 64 AEKIATVGDVAVNYIQN 79
Db 63 AEKIATVGDVAVNYIES 78

RESULT 4
US-10-282-122A-60882
; Sequence 60882, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60882
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60882

Query Match      71.5%; Score 284; DB 4; Length 77;
```

```

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58089
LENGTH: 76
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-282-122A-58089
Query Match          64.0%; Score 254; DB 4; Length 76;
Best Local Similarity 72.2%; Pred. No. 7,le-20;
Matches 52; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY      10 ERYVTKIIVDRIGVDADVVKLEASFKEDLGADSIDVVELVEDEPFMEISDEDPAEKIAT 69
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       5 ERVAKLIVEQLGVBEDEVKPEASFVEDLGADSLDTVELVMALREBFIEIPDEEAERKITT 64
QY      70 VGDANYTIONNQ 81
           |:::|||
Db       65 VQSAIDVQNNO 76
RESULT 7
US-10-282-122A-67443
Sequence 67443, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

```

```
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67443
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-282-122A-67443
```

```
Query Match          62.7%; Score 249; DB 4; Length 76;
Best Local Similarity 70.8%; Pred. No. 2.5e-19;
Matches 51; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
```

```
Qy      10  EKVTKIIVRLGVNDAVYKLEASFKEDLGADSLDVLVWELDEDFPMETISDEDAEKIAT 69
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      5  ERVKKIIVQQLGVNDAVYKLEASFKEDLGADSLDVLVWELDEDFPMETISDEDAEKIAT 64
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      70  VGDVAVNYIQNOQ 81
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      65  VQSAIDYVQNNQ 76
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 8
US-10-282-122A-77373
; Sequence 77373, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
```

```
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 77373
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77373
```

```
Query Match          60.2%; Score 239; DB 4; Length 110;
Best Local Similarity 72.1%; Pred. No. 4.7e-18;
Matches 49; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
```

```
Qy      10  ERVKTKIIVRLGVNDAVYKLEASFKEDLGADSLDVLVWELDEDFPMETISDEDAEKIAT 69
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      38  ERVKKIIVQQLGVNDAVYKLEASFKEDLGADSLDVLVWELDEDFPMETISDEDAEKIAT 97
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      70  VGDVAVNYI 77
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      98  VQSAIDYV 105
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
US-10-282-122A-70919
; Sequence 70919, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
```

```

; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70919
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70919

Query Match          59.9%; Score 238; DB 4; Length 77;
Best Local Similarity 67.1%; Pred. No. 3.8e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLERTKTIIVRLGVDEADVLEASFKEDLGADSLDVLELWLEDEDFMEISDEDAEK 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ENPDKVKDIIIVRLGVDAKVTEDASFKDGLGADSLDIALWLEDEDFGTEIPDEBAEK 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 IATVGDAVNYION 79
    | | | | | | | | | | : : : : : : : : : : : : : : : : : : :
DB 62 INTVGDAVKYINS 74
    | | | | | | | | | | : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-282-122A-71791
; Sequence 71791, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITPA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71791
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
```

```

US-10-282-122A-71791

Query Match          59.9%; Score 238; DB 4; Length 77;
Best Local Similarity 67.1%; Pred. No. 3.8e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLERTKTIIVRLGVDEADVLEASFKEDLGADSLDVLELWLEDEDFMEISDEDAEK 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ENPDKVKDIIIVRLGVDAKVTEDASFKDGLGADSLDIALWLEDEDFGTEIPDEBAEK 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 IATVGDAVNYION 79
    | | | | | | | | | | : : : : : : : : : : : : : : : : : : :
DB 62 INTVGDAVKYINS 74
    | | | | | | | | | | : : : : ~~~~~
    | | | | | | | | | | : : : : ~~~~~

RESULT 11
US-10-724-972A-5601
; Sequence 5601, Application US/10724972A
; Publication No. US2004014734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PAT03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 5601
; LENGTH: 79
; TYPE: PRT
; ORGANISM: S. epidermidis
US-10-724-972A-5601

Query Match          59.9%; Score 238; DB 4; Length 79;
Best Local Similarity 67.1%; Pred. No. 4e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLERTKTIIVRLGVDEADVLEASFKEDLGADSLDVLELWLEDEDFMEISDEDAEK 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 ENPDKVKDIIIVRLGVDAKVTEDASFKDGLGADSLDIALWLEDEDFGTEIPDEBAEK 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 IATVGDAVNYION 79
    | | | | | | | | | | : : : : ~~~~~
DB 64 INTVGDAVKYINS 76
    | | | | | | | | | | : : : : ~~~~~

RESULT 12
US-10-282-122A-51523
; Sequence 51523, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:49, Search time 26.597 Seconds
(without alignments)
251.785 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397

Sequence: 1 GLGSGADTLERVTIKIIVDL.....EDAEKATVGDVAVNTIQNOQ 81

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5.COMB.dep.*

2: /cgn2_6/prodata/1/iaa/6.COMB.dep.*

3: /cgn2_6/prodata/1/iaa/H.COMB.dep.*

4: /cgn2_6/prodata/1/iaa/PCTUS.COMB.dep.*

5: /cgn2_6/prodata/1/iaa/RE.COMB.dep.*

6: /cgn2_6/prodata/1/iaa/backfillseq.dep.*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	81	2	US-09-770-834-1
2	238	59.9	79	2	US-09-134-001C-4809
3	234	58.9	77	2	US-10-089-019-26
4	225	56.7	94	2	US-09-543-681A-7956
5	222.5	56.0	80	2	US-09-902-540-14560
6	215	54.2	77	2	US-09-770-834-15
7	215	54.2	78	2	US-10-089-019-34
8	215	54.2	108	2	US-09-489-039A-7550
9	214	53.9	81	2	US-09-252-991A-18646
10	205	51.6	372	2	US-09-252-991A-30132
11	197	49.6	79	2	US-09-198-452A-308
12	197	49.6	80	2	US-09-438-185A-297
13	188	47.4	99	2	US-09-328-352-4669
14	180	45.3	86	2	US-09-107-532A-7143
15	170	42.8	111	2	US-09-248-796A-17438
16	164.5	41.4	100	2	US-09-902-540-13542
17	160	40.3	101	2	US-09-107-532A-7092
18	158.5	39.9	74	2	US-09-583-110-3914
19	158.5	39.9	74	2	US-10-089-019-30
20	154	38.8	122	2	US-09-248-796A-17437
21	153.5	38.7	77	2	US-09-583-110-4176
22	153.5	38.7	84	2	US-09-107-453-4377
23	148.5	37.4	77	2	US-08-858-207A-302
24	148.5	37.4	77	2	US-10-089-019-28
25	134	33.8	97	2	US-09-602-787A-36
26	134	33.8	97	2	US-09-852-137-2
27	122	30.7	120	2	US-09-056-556-195

28	122	30.7	120	2	US-09-072-596-190	Sequence 190, App
29	122	30.7	120	2	US-09-072-967-195	Sequence 195, App
30	122	30.7	120	2	US-10-193-002-190	Sequence 190, App
31	122	30.7	120	2	US-10-084-843-195	Sequence 195, App
32	106	26.7	136	2	US-08-580-545B-8	Sequence 8, Appli
33	106	26.7	136	2	US-09-262-653A-8	Sequence 8, Appli
34	99.5	25.1	2756	1	US-08-375-709-11	Sequence 11, Appl
35	99.5	25.1	2756	1	US-08-752-929-11	Sequence 11, Appl
36	99.5	25.1	2756	2	US-09-090-793-7	Sequence 7, Appli
37	99.5	25.1	2756	2	US-09-231-899-7	Sequence 7, Appli
38	97	24.4	41	1	US-08-453-924-8	Sequence 8, Appli
39	94	23.7	110	2	US-09-543-681A-6806	Sequence 6806, Ap
40	93.5	23.6	93	2	US-09-266-965-117	Sequence 117, App
41	91.5	23.0	1481	2	US-09-231-899-70	Sequence 70, Appl
42	85.5	21.5	85	2	US-09-902-540-13340	Sequence 13340, A
43	84	21.2	40	1	US-08-129-129-6	Sequence 6, Appli
44	83	20.9	359	2	US-09-266-965-120	Sequence 120, App
45	76	19.1	84	1	US-08-901-306-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT 1
US-09-770-834-1
Sequence 1, Application US/09770834
Patent No. 6684162
GENERAL INFORMATION:
APPLICANT: Patris, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 81
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-770-834-1
Query Match 100.0%; Score 397; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2,8e-40;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLGSGADTLERVTIKIIVDLGVDEADVKKLEAFKEDIGADSDVVELVMELEDFPMETS 60
DB 1 GLGSGADTLERVTIKIIVDLGVDEADVKKLEAFKEDIGADSDVVELVMELEDFPMETS 60
QY 61 DEDAEKATVGDVAVNTIQNOQ 81
DB 61 DEDAEKATVGDVAVNTIQNOQ 81
RESULT 2
US-09-134-001C-4809
Sequence 4809, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
```

FILE REFERENCE: 2368/14

CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 77
TYPE: PRT
ORGANISM: Escherichia coli
US-09-770-834-15

Query Match 54.2%; Score 215; DB 2; Length 77;
Best Local Similarity 63.9%; Pred. No. 1,7e-18;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIIVRLGVDEADVLEASFKEDELGADSLDVLVLMLEDEDFDEISDEDAEKIAT 69
DB 5 ERYVKTIIGSQLGVKEEVNTNNSFVEDLGADSLDVLVLMLEEFDETFEIPDEBAEKITT 64

QY 70 VGDVAVNYIQNOQ 81
DB 65 VQAADIDYINGHQ 76

RESULT 7
US-10-089-019-34
Sequence 34, Application US/10089019
Patent No. 6951729
GENERAL INFORMATION:
APPLICANT: DEMOLF, WALTER E. JR
APPLICANT: KALENDER, HOWARD
APPLICANT: LONSDALE, JOHN T.
TITLE OF INVENTION: METHODS FOR MAKING AND USING FATY ACID
FILE REFERENCE: GM50068
CURRENT APPLICATION NUMBER: US/10/089,019
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/US00/29451
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/161,775
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 78
TYPE: PRT
ORGANISM: Escherichia coli
US-10-089-019-34

Query Match 54.2%; Score 215; DB 2; Length 78;
Best Local Similarity 63.9%; Pred. No. 1,7e-18;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIIVRLGVDEADVLEASFKEDELGADSLDVLVLMLEDEDFDEISDEDAEKIAT 69
DB 6 ERYVKTIIGSQLGVKEEVNTNNSFVEDLGADSLDVLVLMLEEFDETFEIPDEBAEKITT 65

QY 70 VGDVAVNYIQNOQ 81
DB 66 VQAADIDYINGHQ 77

RESULT 8
US-09-489-039A-7550
Sequence 7550, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7550
LENGTH: 108
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7550

Query Match 54.2%; Score 215; DB 2; Length 108;
Best Local Similarity 63.9%; Pred. No. 2,7e-18;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIIVRLGVDEADVLEASFKEDELGADSLDVLVLMLEDEDFDEISDEDAEKIAT 69
DB 36 ERYVKTIIGSQLGVKEEVNTNNSFVEDLGADSLDVLVLMLEEFDETFEIPDEBAEKITT 95

QY 70 VGDVAVNYIQNOQ 81
DB 96 VQAADIDYINGHQ 107

RESULT 9
US-09-252-991A-18646
Sequence 18646, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18646
LENGTH: 81
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18646

Query Match 53.9%; Score 214; DB 2; Length 81;
Best Local Similarity 59.0%; Pred. No. 2,4e-18;
Matches 46; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 4 GSADTLERYTKIIIVRLGVDEADVLEASFKEDELGADSLDVLVLMLEDEDFDEISDESD 63
DB 3 GMSITTEERYKTIIVASQLGVKEEVNTNNSFVEDLGADSLDVLVLMLEEFDETFEIPDEBAEKITT 62

QY 64 AEKIATVGDVAVNYIQNOQ 81
DB 63 AEKITTVEAIDYIAHQ 80

RESULT 10
US-09-252-991A-30132
Sequence 30132, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30132
LENGTH: 372
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30132

Query Match 51.6%; Score 205; DB 2; Length 372;
Best Local Similarity 50.0%; Pred. No. 2.2e-16;
Matches 39; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 GFLGSADTLERYTKIIVDRIGVDADVKLEASFKEDLGADSLDVVELVMELEDFDMEIS 60
DB 290 GQGCMDITFRKVLVAARFVECDIRLDSFRNDFGASLEVELVWALFAAFGEVLA 349

QY 61 DDAEKIATVGDAVNYIQ 78
DB 350 DDAERIEFVROAIDYLE 367

RESULT 11
US-09-198-452A-308
Sequence 308, Application US/09198452A
Patent No. 6559294

GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 308
LENGTH: 79
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-308

Query Match 49.6%; Score 197; DB 2; Length 79;
Best Local Similarity 57.1%; Pred. No. 2.5e-16;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 12 VKKIIVDRIGVDADVKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAEKIATVG 71
DB 7 VIAIIVEQLGVDPKEVENSFFIEDLNADSLDTLITLIEKFAFISEDAEKLRITVG 66

QY 72 DAVNYIONQO 81
DB 67 DVFTYIKKRQ 76

RESULT 12
US-09-438-185A-297
Sequence 297, Application US/09438185A
Patent No. 6822071

GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 297

LENGTH: 80
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: Cpn0295
US-09-438-185A-297

Query Match 49.6%; Score 197; DB 2; Length 80;
Best Local Similarity 57.1%; Pred. No. 2.6e-16;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 12 VKKIIVDRIGVDADVKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAEKIATVG 71
DB 8 VIAIIVEQLGVDPKEVENSFFIEDLNADSLDTLITLIEKFAFISEDAEKLRITVG 67

QY 72 DAVNYIONQO 81
DB 68 DVFTYIKKRQ 77

RESULT 13
US-09-328-352-4669
Sequence 4669, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4669
LENGTH: 99
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4669

Query Match 47.4%; Score 188; DB 2; Length 99;
Best Local Similarity 48.6%; Pred. No. 4.1e-15;
Matches 35; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 6 ADTLERVTKIIVDRIGVDADVKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 65
DB 23 SDIERQVQAAVEQLGKAERIKNEASFMDDLGADSLDVVELVWVSPFNDPITIPDEDSN 82

QY 66 KIATVGDAVNYI 77
DB 83 EITVQSAIDVY 94

RESULT 14
US-09-107-532A-7143
Sequence 7143, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A. Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

This Page Blank (uspto)

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:34 ; Search time 118.075 Seconds
(without alignments)
483.997 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397
Sequence: 1 GPLGSADTLERVTKIIVDRLL.....EDAEKIAIVGDAVNTYQNOQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_spdoc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	370	93.2	77	1	ACP_BACSU	P80643 bacillus su
2	345	86.9	77	2	Q65706_BACLD	Q65706 bacillus li
3	315	79.3	77	2	Q51004_GEOXA	Q51004 geobacillus
4	313	78.8	77	1	ACP_BACDZ	Q9ka04 bacillus ha
5	311	78.3	77	1	ACP_BACSK	Q5wf55 bacillus cl
6	302	76.1	77	1	ACP_BACAN	Q81w17 bacillus an
7	302	76.1	77	1	ACP_BACCI	Q732a0 bacillus ce
8	302	76.1	77	1	ACP_BACCR	Q819v7 bacillus ce
9	302	76.1	77	1	ACP_BACDZ	Q636h6 bacillus ce
10	302	76.1	77	1	ACP_BACCH	Q6hew5 bacillus th
11	302	76.1	77	2	Q4MH03_BACCE	Q634d0 listeria in
12	284	71.5	77	1	ACP_LISIN	Q71y10 listeria mo
13	284	71.5	77	1	ACP_LISMF	Q63439 listeria mo
14	284	71.5	77	1	ACP_LISMO	Q6hew5 bacillus th
15	271	68.3	77	1	ACP_OCEIH	Q636h6 bacillus ce
16	254	64.0	76	1	ACP_HAEIN	Q636h6 bacillus ce
17	254	64.0	76	1	ACP_HAEIN	Q636h6 bacillus ce
18	254	64.0	76	2	Q4OF33_HABE8	Q636h6 bacillus ce
19	249	62.7	76	1	ACP_PASNU	Q636h6 bacillus ce
20	249	62.7	76	1	Q67PF6_SYMPH	Q636h6 bacillus ce
21	247	62.2	77	2	Q4VK22_VIBAN	Q636h6 bacillus ce
22	244	61.5	76	1	ACP_VIBHA	Q636h6 bacillus ce
23	244	61.5	76	1	ACP_VIBHA	Q636h6 bacillus ce
24	243	61.2	77	2	Q5E412_VIBF1	Q636h6 bacillus ce
25	239	60.2	77	1	ACP_VIBCH	Q636h6 bacillus ce
26	238	59.9	77	1	ACP_STAEP	Q636h6 bacillus ce
27	238	59.9	77	2	Q4L574_STAHI	Q636h6 bacillus ce
28	238	59.9	77	2	Q5HPV9_STAEO	Q636h6 bacillus ce
29	236	59.4	77	1	ACP_CIOAB	Q636h6 bacillus ce
30	236	59.4	77	1	ACP_VIBVU	Q636h6 bacillus ce
31	236	59.4	78	1	ACP_VIBVY	Q636h6 bacillus ce

32	235	59.2	77	1	ACP_HAEIU	Q7vk6 haemophilus
33	234	58.9	77	1	ACP_STAAM	P0a001 staphylococ
34	234	58.9	77	1	ACP_STAAM	P0a002 staphylococ
35	234	58.9	77	1	ACP_STAAR	Q6ghk3 staphylococ
36	234	58.9	77	1	ACP_STAAS	Q6g9y1 staphylococ
37	234	58.9	77	1	ACP_STAAM	P0a003 staphylococ
38	234	58.9	77	2	Q5HGK0_STPAC	Q6g9y1 staphylococ
39	233	58.7	76	1	ACP_THETN	Q8x9w1 thermococ
40	233	58.7	78	2	Q7N387_PHOHL	Q7a387 photorhabd
41	232	58.4	78	1	ACP_PHOER	Q9r6z3 photobacter
42	231	58.2	79	2	Q5QZ23_IDIIL	Q5qz23 idiomarina
43	230	57.9	77	1	ACP_GEOSL	Q7a387 photobacter
44	230	57.9	77	1	ACP_LEPIC	Q7a387 photobacter
45	230	57.9	77	1	ACP_LEPIN	Q8exx4 leptospira

ALIGNMENTS

RESULT 1	ACP_BACSU	STANDARD;	PRT;	77 AA.
AC	P80643; P51832;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	ACP carrier protein (ACP).			
GN	Name=acpA; Synonyms=acpP; Ordered locus names=BSU15920;			
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			
RP	PROTEIN SEQUENCE OF 15-77, AND NUCLEOTIDE SEQUENCE OF 1-14.			
RC	STRAIN=168;			
RX	MEDLINE=96257247; PubMed=8654983; DOI=10.1016/0378-1119(96)00181-3;			
RT	"The effect of Str, a homologue of the mammalian SRP receptor alpha-subunit, on Bacillus subtilis growth and protein translocation."			
RT	Gene 172:17-24(1996).			
RL	[3]			
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RP	STRAIN=168;			
RX	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;			
RT	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bortner M.G., Bessieres P., Bolotin A., Borchert S., Bortner R., Bortner L., Brans A., Braun M., Brignelli S.C., Bron S., Brouillet S., Brusch C.V., Caldwell I.F., Cummings N.J., Daniel R.A., Choi S.-K., Codani U.-J., Cornerton I.F., Ehlrich S.D., Emerson P.T., Deniot F., Devine K.M., Duesterhoeft A., Ehlrich S.D., Emerson P.T., Britton K.-D., Brington J., Fabre C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.-Y., Glaser P., Goffeau A., Golligly E.J., Grandi G., Guiseppe G., Guy B.J., Haga K., Hatach J., Harwood C.R., Henaut A., Hilbert H., Holtsappel S., Hosono S., Hullo M.-F., Itaya M., Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krog S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C., Medine C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.-H., Patro V., Pohl T.M., Portecelle D., Porrolik S., Prescott A.M., Presseau E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,			

RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpsstra P.,
 RA Tokomai A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vassarotti A., Viari A., Wandut R., Wedler E., Wedler H.,
 RA Welzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zimstein E.,
 RA Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
 RT Nature 390:249-256 (1997).
 RN [4]
 RN PROTEIN SEQUENCE OF 1-17.
 RP MEDLINE=94131947; PubMed=8300523;
 RX Heaton M.P., Neuhaus F.C.;
 RA "Role of the D-alanyl carrier protein in the biosynthesis of D-alanyl-
 RT lipoteichoic acid,"
 RT J. Bacteriol. 176:681-690 (1994).
 RL [5]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HOLO-(ACYL CARRIER PROTEIN)
 RP IN COMPLEX WITH HOLO-(ACYL CARRIER PROTEIN) SYNTHASE.
 RX PubMed=10997907; DOI=10.1016/S0969-2126(00)00178-7
 RA Pareis K.D., Lin L., Tam A., Mathew R., Hixon J., Stahl M.,
 RA Fritz C.C., Seehra J., Somers W.S.;
 RT "Crystal structures of substrate binding to *Bacillus subtilis* holo-
 RT (acyl carrier protein) synthase reveal a novel trimeric arrangement of
 RT molecules resulting in three active sites,"
 RT Structure 8:883-895 (2000).
 RN [6]
 RN STRUCTURE BY NMR.
 RP MEDLINE=21416009; PubMed=11525165; DOI=10.1016/S0969-2126(01)00586-X;
 RX Xu G.-Y., Tam A., Lin L., Hixon J., Fritz C.C., Powers R.;
 RA "Solution structure of *B. subtilis* acyl carrier protein,"
 RT Structure 9:277-287 (2001).
 RL -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis.
 CC -1- PATHWAY: De novo fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC serine of apo-ACP by acps. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulhydryl of the prosthetic group.
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U59433; AAC44308.1; -; Genomic DNA.
 DR EMBL; D64116; BAA10975.1; -; Genomic DNA.
 DR EMBL; Z59112; CAB13465.1; -; Genomic DNA.
 DR PIR; JC4822; JC4822.
 DR PIR; T46634; T46634.
 DR PDB; 1F80; X-ray; D/E/F=-.
 DR PDB; 1H80; NMR; A=2-77.
 DR Subtilisin; BG1536; acpA.
 DR HAMAP; MF_01217; -; 1.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR003231; Acyl carrier.
 DR InterPro; IPR006163; Phosphopanteth_bd.
 DR InterPro; IPR006162; Pantane_S.
 DR Pfam; PF00550; PP-binding; 1.
 DR ProDom; PD000887; Acyl_carrier; 1.
 DR TIGRfam; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 DR PROSITE; PS50012; PHOSPHOPANTETHEINE; 1.
 KW 3D-structure; Complete proteome; Direct protein sequencing;
 KW Fatty acid biosynthesis; Lipid synthesis; Phosphopantetheine.
 FT BINDING 37 37 Phosphopantetheine (covalent).
 FT HELIX 3 16
 FT TURN 25 26
 FT STRAND 26 28

FT HELIX 29 33
 FT HELIX 37 50
 FT TURN 51 52
 FT HELIX 57 61
 FT TURN 62 62
 FT STRAND 65 65
 FT HELIX 66 74
 SQ SEQUENCE 77 AA; 8591 MW; 75E745DE3C6A0951 CRC64;
 Query Match 93.2%; Score 370; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 6.1e-24;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ADLTERVTKIVDPVGVDEADVKLEASPKEDLGADSLDVELVMELEDEPFMEISDEDAE 65
 DB 2 ADLTERVTKIVDPVGVDEADVKLEASPKEDLGADSLDVELVMELEDEPFMEISDEDAE 61
 QY 66 KIATVGDAVNYIQNQ 81
 DB 62 KIATVGDAVNYIQNQ 77
 RESULT 2
 ID 065J06 BACLD PRELIMINARY; PRT; 77 AA.
 AC 065J06; 062V61;
 DT 25-OCT-2004 (TRENBLREL. 28, Created)
 DT 25-OCT-2004 (TRENBLREL. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
 DE ACPA (acyl carrier protein).
 GN Name:acpa; OrderedLocName=BL02316; BL010813;
 OS *Bacillus licheniformis* (strain DSM 13 / ATCC 14580).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 CC NCBI_Taxid=279010;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=15383718; DOI=10.1159/000079829;
 RX Velth B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baerner S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gotschalk G.;
 RT "The complete genome sequence of *Bacillus licheniformis* DSM13, an
 RT organism with great industrial potential,"
 RT J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
 RX Rey M.W., Kamaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
 RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
 RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Gatteron N.,
 RA Ehrlich S.D., Berkas R.M.;
 RT "Complete genome sequence of the industrial bacterium *Bacillus licheniformis* and comparisons with closely related *Bacillus* species,"
 RT Genome Biol. 5:RESEARCH077.1-RESEARCH077.12 (2004).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 CC EMBL; AE017333; AAU40708.1; -; Genomic DNA.
 CC EMBL; CP000002; AAU23348.1; -; Genomic DNA.
 DR SMR; Q65J06; 2-77.
 DR GO; GO:000036; F:acyl carrier activity; IEA.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR003231; Acyl_carrier.
 DR InterPro; IPR006163; Phosphopanteth_bd.
 DR InterPro; IPR006162; Pantane_S.
 DR Pfam; PF00550; PP-binding; 1.
 DR ProDom; PD000887; Acyl_carrier; 1.
 DR TIGRfam; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 DR PROSITE; PS50012; PHOSPHOPANTETHEINE; 1.
 KW Complete proteome; Phosphopantetheine.
 SQ SEQUENCE 77 AA; 8493 MW; 9AFDA53DBC6C033C CRC64;

Query Match 86.9%; Score 345; DB 2; Length 77;
 Best Local Similarity 93.4%; Pred. No. 86-22;
 Matches 71; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 ADLTERVTKIYDRGLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 65
 DB 2 ADALERTVTKIYDRGLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 61
 QY 66 KIATVGDAVNYIQNQ 81
 DB 62 KIATVGDAVNYIKSR 77

RESULT 3
 OS1004_GEOKA PRELIMINARY; PRT; 77 AA.

AC OS1004; 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN OrderedLocuNames=GK1191;
 OS Geobacillus kaustophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1462; [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=HTM426;
 RC PubMed=1576355; DOI=10.1093/nar/gkh970;
 RX Takami H., Takaki Y., Chee G.-Y., Nishi S., Shimamura S., Suzuki H.,
 RA Matsui S., Uchiyama I.;
 RA "Thermoadaptation trait revealed by the genome sequence of
 RT thermophilic Geobacillus kaustophilus";
 RL Nucleic Acids Res. 32:6292-6303(2004).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 DR EMBL; BA000043; BAD75476.1; -; Genomic_DNA.
 DR SMR; OS1004; 2-76.
 DR GO; GO:0000036; F:acyl carrier activity; IEA.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
 DR GO; GO:0006633; F:fatty acid biosynthesis; IEA.
 DR GO; GO:0006323; A:acyl carrier.
 DR InterPro; IPR006163; Phspanteth_bind.
 DR InterPro; IPR006162; Phantne_S.
 DR Pfam; PF00550; PP-binding_1.
 DR ProDom; PD000867; Acyl_carrier; 1.
 DR TIGRfams; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS00075; ACP_DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 KW Complete proteome; Phosphopantetheine.
 SQ SEQUENCE 77 AA; 8619 MW; C47CC8C7BCF4BA4C CRC64;

Query Match 79.3%; Score 315; DB 2; Length 77;
 Best Local Similarity 84.0%; Pred. No. 2-7e-19;
 Matches 63; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 6 ADLTERVTKIYDRGLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 65
 DB 2 ADLTERVTKIYDRGLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 61
 QY 66 KIATVGDAVNYIQNQ 80
 DB 62 KIATVGDAVNYIKSR 76

RESULT 4
 ACP_BACHD STANDARD; PRT; 77 AA.
 ID ACP_BACHD
 AC OSKAO4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Acyl carrier protein (ACP).
 GN Name=acpP; Synonyms=acpA; OrderedLocuNames=BH2490;
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665; [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11056132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis (By similarity).
 CC -1- PATHWAY: De novo fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC serine of apo-ACP by acpS. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulphydryl of the prosthetic group (By similarity).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; BA000004; BAB06209.1; -; Genomic_DNA.
 DR PIR; B83961; B83961.
 DR HSSP; P80643; 1HY8.
 DR SMR; OSKAO4; 2-77.
 DR HAMAP; MF_01217; -; 1.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR003221; Acyl_carrier.
 DR InterPro; IPR006163; Phosphopanteth_bd.
 DR InterPro; IPR006162; Phantne_S.
 DR Pfam; PF00550; PP-binding_1.
 DR ProDom; PD000867; Acyl_carrier; 1.
 DR TIGRfams; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS00075; ACP_DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 DR Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine.
 FT BINDING 37 Phosphopantetheine (covalent) (By
 FT similarity).
 SQ SEQUENCE 77 AA; 8558 MW; 3575CDFA45BA15CA CRC64;

Query Match 78.8%; Score 313; DB 1; Length 77;
 Best Local Similarity 81.6%; Pred. No. 4e-19;
 Matches 62; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 6 ADLTERVTKIYDRGLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 65
 DB 2 ADLTERVTKIYDRGLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAE 61
 QY 66 KIATVGDAVNYIQNQ 81
 DB 62 KIATVGDAVNYIEGRQ 77

RESULT 5
 ACP_BACSK STANDARD; PRT; 77 AA.
 ID ACP_BACSK
 AC OSWFM5;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN Name=acpP; Synonyms=acpA; OrderedLocuNames=ABC3300;

OS Bacillus clausii (strain KSM-K16).
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxId=66692;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Takaki Y., Kaseyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RA "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: AP006627; BMD64835.1; -; Genomic_DNA.
CC SMR: Q5WFM5; 2-77.
DR HAMAP: MF_01217; -; 1.
DR InterPro: IPR009081; ACP like.
DR InterPro: IPR003211; Acyl carrier.
DR InterPro: IPR006163; Phosphopanteth_bd.
DR InterPro: IPR006162; Pantne_S.
DR Pfam: PF00550; PP-binding; 1.
DR ProDom: PD000887; Acyl carrier; 1.
DR TIGRFAMs: TIGR00517; acyl carrier; 1.
DR PROSITE: PS00075; ACP DOMAIN; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; FALSE NEG.
KM Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Phosphopantetheine.
FT BINDING 37 Phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8795 MW; C52A0886379B9150 CRC64;
Query Match 78.3%; Score 311; DB 1; Length 77;
Best Local Similarity 82.9%; Pred. No. 6e-19;
Matches 63; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 6 ADLLEKTVKIIYRLGVDEADYKLEASFKEDLGADSLDVVELVMELEDFEIDEDEDAE 65
DB 2 ADVMEKVTIIVDRLGVESESVLESSFEDLKADSLDVVELVMELEDFEIDEDEDAE 61
QY 66 KIATVGDVAVYIIONQ 81
DB 62 KIATVGDVAVYIIONQ 77
RESULT 6
ACP_BACAN STANDARD; PRT; 77 AA.
ID_ACP_BACAN
AC 081W17; G6HUN6; G6KNW9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acp; Synonyms=acpa; OrderedLocustNames=BA3988, GBA3988, BAS3701;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OK NCBI_TaxId=1392;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames / isolate Porton;

RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillye L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin N., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgeson E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Twatle J.E., White O.,
RA Salberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RA "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN (2)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Fedorova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RA "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN (3)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinka R.,
RA Richardson P., Rubin E., Rice H.;
RA "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: AE017036; AAP27716.1; -; Genomic_DNA.
CC EMBL: AE017334; AAT33103.1; -; Genomic_DNA.
CC EMBL: AE017225; AAT56003.1; -; Genomic_DNA.
CC HSSP: P80643; 1P80.
DR SMR: Q81W17; 2-76.
DR TIGR: BA3988; -;
DR TIGR: GBA3988; -;
DR HAMAP: MF_01217; -; 1.
DR InterPro: IPR009081; ACP like.
DR InterPro: IPR003211; Acyl carrier.
DR InterPro: IPR006163; Phosphopanteth_bd.
DR InterPro: IPR006162; Pantne_S.
DR Pfam: PF00550; PP-binding; 1.
DR ProDom: PD000887; Acyl carrier; 1.
DR TIGRFAMs: TIGR00517; acyl carrier; 1.
DR PROSITE: PS00075; ACP DOMAIN; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; 1.
KM Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Phosphopantetheine.
FT BINDING 37 Phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8513 MW; BCCA3CBAB5DA0A0B CRC64;
Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
QY 6 ADLTERVTKIIVRLGVDEADVKLKASFKEDLGADSLDVLELVMELEDFEPMISDEDAE 65
DB 2 ADLTERVTKIIVRLGVDEADVKLKASFKEDLGADSLDVLELVMELEDFEPMISDEDAE 61
QY 66 KIATVGDAVNYION 79
DB 62 KIATVGDAVNYIES 75

RESULT 7
AC  AC_BACCI STANDARD; PRT; 77 AA.
ID  AC_BACCI
AC  0732M0;
DT  10-MAY-2005 (Rel. 47, Created)
DT  10-MAY-2005 (Rel. 47, Last sequence update)
DE  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Acyl carrier protein (ACP).
GN  Name=acpP; Synonyms=acpA; OrderedLocustNames=BC3892;
OS  Bacillus cereus (strain ATCC 10987).
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC  Bacillus cereus group.
OX  NCBI_TaxID=225253;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX  PubMed=14960714; DOI=10.1093/nar/gkh258;
RA  Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA  Shores K.A., Fouts D.E., Tourasse N.J., Angiolini S.V., Kolonay J.F.,
RA  Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT  "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT  adaptations and a large plasmid related to Bacillus anthracis pXOI."
RL  Nucleic Acids Res. 32:977-988(2004).
CC  -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC  biosynthesis (By similarity).
CC  -1- PATHWAY: De novo fatty acid biosynthesis.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC  serine of apo-ACP by acps. This modification is essential for
CC  activity because fatty acids are bound in thioester linkage to the
CC  sulphydryl of the prosthetic group (By similarity).
CC  -1- SIMILARITY: Contains 1 acyl carrier domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; AE017276; AAS42797.1; -; Genomic_DNA.
DR  HSSP; P02901; IACP.
DR  SMR; Q732M0; 2-76.
DR  TIGR; BCE3892; -.
DR  HAMAP; MF_01217; -; 1.
DR  InterPro; IPR009081; ACP like.
DR  InterPro; IPR003231; Acyl carrier.
DR  InterPro; IPR006163; Phosphopanteth_b.
DR  InterPro; IPR006162; Ppantne_S.
DR  Pfam; PF00550; PP-binding; 1.
DR  ProDom; PD000887; Acyl carrier; 1.
DR  TIGRFAMs; TIGR00517; acyl carrier; 1.
DR  PROSITE; PS50075; ACP DOMAIN; 1.
DR  PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
KW  Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW  Phosphopantetheine.
FT  BINDING 37 Phosphopantetheine (covalent) (By
FT similarity)
SQ  SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;
Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 6 ADLTERVTKIIVRLGVDEADVKLKASFKEDLGADSLDVLELVMELEDFEPMISDEDAE 65
DB 2 ADLTERVTKIIVRLGVDEADVKLKASFKEDLGADSLDVLELVMELEDFEPMISDEDAE 61
QY 66 KIATVGDAVNYION 79
DB 62 KIATVGDAVNYIES 75

RESULT 8
AC  AC_BACCR STANDARD; PRT; 77 AA.
ID  AC_BACCR
AC  0819V7;
DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DE  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Acyl carrier protein (ACP).
GN  Name=acpP; OrderedLocustNames=BC3848;
OS  Bacillus cereus (strain ATCC 14579 / DSM 31).
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC  Bacillus cereus group.
OX  NCBI_TaxID=226900;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX  MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA  Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA  Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA  Chu L., Mazur M., Goldsman E., Larsen N., P'Souza M., Walunas T.,
RA  Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA  Overbeek R., Kyriades N.C.;
RT  "Genome sequence of Bacillus cereus and comparative analysis with
RT  Bacillus anthracis."
RL  Nature 423:87-91(2003).
CC  -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC  biosynthesis (By similarity).
CC  -1- PATHWAY: De novo fatty acid biosynthesis.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC  serine of apo-ACP by acps. This modification is essential for
CC  activity because fatty acids are bound in thioester linkage to the
CC  sulphydryl of the prosthetic group (By similarity).
CC  -1- SIMILARITY: Contains 1 acyl carrier domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; AE017010; AAP10770.1; ALT_INIT; Genomic_DNA.
DR  HSSP; P80643; 1F80.
DR  SMR; Q819V7; 2-76.
DR  HAMAP; MF_01217; -; 1.
DR  InterPro; IPR009081; ACP like.
DR  InterPro; IPR003231; Acyl carrier.
DR  InterPro; IPR006163; Phosphopanteth_b.
DR  InterPro; IPR006162; Ppantne_S.
DR  Pfam; PF00550; PP-binding; 1.
DR  ProDom; PD000887; Acyl carrier; 1.
DR  TIGRFAMs; TIGR00517; acyl carrier; 1.
DR  PROSITE; PS50075; ACP DOMAIN; 1.
DR  PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
KW  Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW  Phosphopantetheine.
FT  BINDING 37 Phosphopantetheine (covalent) (By
FT similarity)
SQ  SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;
Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
Db          2  ADVLERVTKIIVDRIGVETEVVPAASFKEIDLGDLSLIVLWQLEDFEFMEISDEDAE 61
QY          66  KIATVGDAVNTYION 79
Db          62  KIATVGDAVNTYIES 75

RESULT 9
ACP_BACCH  STANDARD;          PRT;          77 AA.
ID_ACP_BACCH  Q636H6;
AC  Q636H6;
DT  10-MAY-2005 (Rel. 47, Created)
DT  10-MAY-2005 (Rel. 47, Last sequence update)
DE  10-MAY-2005 (Rel. 47, Last annotation update)
DE  ACP1 carrier protein (ACP).
GN  Name=acpP; Synonyms=acpA; OrderedLocustNames=BCZK3609;
OS  Bacillus cereus (strain ZK).
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC  Bacillus cereus group.
OX  NCBI_TaxID=288681;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA  Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA  Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA  Richardson P., Rubin E., Tice H.;
RT  "Complete genome sequence of Bacillus cereus ZK."
RT  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC  biosynthesis (By similarity).
CC  -1- PATHWAY: De novo fatty acid biosynthesis.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC  serine of apo-ACP by acps. This modification is essential for
CC  activity because fatty acids are bound in thioester linkage to the
CC  sulfhydryl of the prosthetic group (By similarity).
CC  -1- SIMILARITY: Contains 1 acyl carrier domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; CP000001; AAU1654.1; -; Genomic_DNA.
DR  SMR; Q636H6; 2-76.
DR  HAMAP; MF_01217; -; 1.
DR  InterPro; IPR009081; ACP_like.
DR  InterPro; IPR003231; Acyl_carrier.
DR  InterPro; IPR006163; Phosphopanteth_bd.
DR  InterPro; IPR006162; Pantane_S.
DR  Pfam; PF00550; PP-binding; 1.
DR  ProDom; PD000887; Acyl_carrier; 1.
DR  TIGRFAMs; TIGR00517; acyl_carrier; 1.
DR  PROSITE; PS50075; ACP_DOMAIN; 1.
DR  PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW  Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW  Phosphopantetheine.
FT  BINDING          37          Phosphopantetheine (covalent) (By
FT                               similarity).
SQ  SEQUENCE          77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;

Query Match          76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
RESULT 10
ACP_BACCH  STANDARD;          PRT;          77 AA.
ID_ACP_BACCH  Q6H6W5;
AC  Q6H6W5;
DT  10-MAY-2005 (Rel. 47, Created)
DT  10-MAY-2005 (Rel. 47, Last sequence update)
DE  10-MAY-2005 (Rel. 47, Last annotation update)
DE  ACP1 carrier protein (ACP).
GN  Name=acpP; Synonyms=acpA; OrderedLocustNames=Bt9727_3591;
OS  Bacillus thuringiensis (subsp. konkukian).
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC  Bacillus cereus group.
OX  NCBI_TaxID=180856;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=97-27;
RA  Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA  Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA  Richardson P., Rubin E., Tice H.;
RT  "Complete genome sequence of Bacillus thuringiensis 97-27."
RT  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC  biosynthesis (By similarity).
CC  -1- PATHWAY: De novo fatty acid biosynthesis.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC  serine of apo-ACP by acps. This modification is essential for
CC  activity because fatty acids are bound in thioester linkage to the
CC  sulfhydryl of the prosthetic group (By similarity).
CC  -1- SIMILARITY: Contains 1 acyl carrier domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; AE017355; AAT61346.1; -; Genomic_DNA.
DR  SMR; Q6H6W5; 2-76.
DR  HAMAP; MF_01217; -; 1.
DR  InterPro; IPR009081; ACP_like.
DR  InterPro; IPR003231; Acyl_carrier.
DR  InterPro; IPR006163; Phosphopanteth_bd.
DR  InterPro; IPR006162; Pantane_S.
DR  Pfam; PF00550; PP-binding; 1.
DR  ProDom; PD000887; Acyl_carrier; 1.
DR  TIGRFAMs; TIGR00517; acyl_carrier; 1.
DR  PROSITE; PS50075; ACP_DOMAIN; 1.
DR  PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW  Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW  Phosphopantetheine.
FT  BINDING          37          Phosphopantetheine (covalent) (By
FT                               similarity).
SQ  SEQUENCE          77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;

Query Match          76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
RESULT 11
Q4MH03_BACCE  PRELIMINARY;          PRT;          77 AA.
ID  Q4MH03;
AC  Q4MH03;
```

```

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Acyl carrier protein.
GN Name=acpP; ORFNames=BCE_G9241_3833;
OS Bacillus cereus G9241;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RA PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Flitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Baker M., Jiang L., Cer R.Z.,
RA Riletone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -1- FUNCTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAEK0100080; EAL11450.1; -; Genomic_DNA.
CC SEQ SEQUENCE 77 AA; 8513 MW; 8CCACJBASDA0AB CRC64;

Query Match 76.1%; Score 302; DB 2; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 ADTLEKVTIIVDRIGVDADVKLEASFKEDLGADSLDVLELWMELEDFPMEISDEDAE 65
DB 2 ADVLEKVTIIVDRIGVETEVPVPAASFREDLGADSLDVLELWMELEDFPMEISDEDAE 61
QY 66 KIATVGDAVNYIQ 79
DB 62 KIATVGDAVNYIES 75

RESULT 12
ACP_LISIN STANDARD; PRT; 77 AA.
ID _ACP_LISIN STANDARD; PRT; 77 AA.
AC P63440; Q92AK2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; Synonyms=acpA; OrderedLocustNames=lin1920;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIP 11262 / Serovar 6a;
RA MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangoul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duesurget O.,
RA Entian K.-D., Fain H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Maduno E., Maitounan A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species."
CC Science 294:849-852(2001).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

```

```

CC -1- PPM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL596170; CAC97150.1; -; Genomic_DNA.
CC PIR; A1672; A1672.
CC HSSP; P80643; 1H78.
CC SMR; P63440; 2-74.
CC ListList; LIND01920; -.
CC HAMAP; MF_01217; -; 1.
CC InterPro; IPR009081; ACP_1like.
CC InterPro; IPR006163; Phosphopantethe_
CC InterPro; IPR003231; Acyl_carrier.
CC Pfam; PF00550; pp-binding; 1.
CC ProDom; PD000887; Acyl_carrier; 1.
CC TIGRFAMs; TIGR00517; acyl_carrier; 1.
CC PROSITE; PS00075; ACP_DOMAIN; 1.
CC PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
CC Complete proteome; Fatty acid biosynthesis; lipid synthesis;
CC Phosphopantetheine.
CC BINDING 37 Phosphopantetheine (covalent) (By
CC similarity).
CC FT 37
CC SEQ SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;

Query Match 71.5%; Score 284; DB 1; Length 77;
Best Local Similarity 80.8%; Pred. No. 1.1e-16;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTLEKVTIIVDRIGVDADVKLEASFKEDLGADSLDVLELWMELEDFPMEISDEDAE 65
DB 2 AEVLEKVTIIVDRIGVESKVLLEASFKEDLGADSLDVLELWMELEDFPMEISDEDAE 61
QY 66 KIATVGDAVNYIQ 78
DB 62 NINTVGDAVKIE 74

RESULT 13
ACP_LISMF STANDARD; PRT; 77 AA.
ID _ACP_LISMF STANDARD; PRT; 77 AA.
AC Q71YU0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; OrderedLocustNames=LMOF2365_1834;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nielsen M.C., Beanan M.J.,
RA Brinkak L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Katharou S., Wonderling L.D., Unlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species."
CC Nucleic Acids Res. 32:2386-2395(2004).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid

```

```
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL: AE017328; AAT04604.1; -, Genomic_DNA.
CC HSSP: P02901; IACP.
CC SMR: Q71YL0; 2-74.
CC TIGR: LMOF2365.1834; -.
CC HAMAP: MF_01217; -, 1.
CC InterPro: IPR009081; ACP_like.
CC InterPro: IPR003231; Acyl_carrier.
CC InterPro: IPR006163; Phosphopanteth_bd.
CC InterPro: IPR006162; Pantane_S.
CC Pfam: PF00550; PP-binding; 1.
CC ProDom: PD000887; Acyl_carrier; 1.
CC TIGRfam: TIGR00517; acyl_carrier; 1.
CC PROSITE: PS50075; ACP_DOMAIN; 1.
CC PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.
CC Complete proteome: Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
FT BINDING 37 37 Phosphopantetheine (covalent) (By
SQ SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;
similarity)
Query Match 71.5%; Score 284; DB 1; Length 77;
Best Local Similarity 80.8%; Pred. No. 1.1e-16;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTLEKVTKIIVDRIGVDADYKLEASFKEDLGADSLDVLVLMLEDFEPMETSDAE 65
DB 2 AEVLEKVTKIIVDRIGVRESKVTLEASFKEIDLGLADSLDVLVLMLEDFEFGVEISDGA 61
QY 66 KIATVGDVAVNYIQ 78
DB 62 NINTVGDVAVKYIE 74

RESULT 14
ACP LISMO
ID _ACP LISMO STANDARD; PRT; 77 AA.
AC P63439; Q92AK2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP)
GN Name=acpP; Synonyms=acpA; OrderedLocusNames=lmo1806;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BGD-e / Serovar 1/2a; PubMed=11679669; DOI=10.1126/science.1063447;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangoul L., Buchrieser C., Ruhnlok C., Amend A.,
RA Baquero F., Berche P., Blocher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Cove E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Entian K.-D., Falhi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
```

```
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RL Science 294:849-852(2001).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL: AL591981; CAC99884.1; -, Genomic_DNA.
CC FIR: AF1300; AF1300.
CC HSSP: P80643; IHX8.
CC SMR: P63439; 2-74.
CC ListerList: LMO01806; -.
CC HAMAP: MF_01217; -, 1.
CC InterPro: IPR009081; ACP_like.
CC InterPro: IPR003231; Acyl_carrier.
CC InterPro: IPR006163; Phosphopanteth_bd.
CC InterPro: IPR006162; Pantane_S.
CC Pfam: PF00550; PP-binding; 1.
CC ProDom: PD000887; Acyl_carrier; 1.
CC TIGRfam: TIGR00517; acyl_carrier; 1.
CC PROSITE: PS50075; ACP_DOMAIN; 1.
CC PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.
CC Complete proteome: Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
FT BINDING 37 37 Phosphopantetheine (covalent) (By
SQ SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;
similarity)
Query Match 71.5%; Score 284; DB 1; Length 77;
Best Local Similarity 80.8%; Pred. No. 1.1e-16;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTLEKVTKIIVDRIGVDADYKLEASFKEDLGADSLDVLVLMLEDFEPMETSDAE 65
DB 2 AEVLEKVTKIIVDRIGVRESKVTLEASFKEIDLGLADSLDVLVLMLEDFEFGVEISDGA 61
QY 66 KIATVGDVAVNYIQ 78
DB 62 NINTVGDVAVKYIE 74

RESULT 15
ACP OCEIH
ID _ACP OCEIH STANDARD; PRT; 77 AA.
AC Q8ER06;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; OrderedLocusNames=OB1525;
OS Oceanobacillus thelyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=HT5831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=1235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.,
RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
```

```

RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000028; BAC13481.1; -; Genomic_DNA.
CC HSSP; P80643; 1F80.
CC SMR; OBER06; 2-76.
CC HAMAP; MF_01217; -; 1.
CC InterPro; IPR009081; ACP like.
CC InterPro; IPR003231; Acyl_carrier.
CC InterPro; IPR006163; Phosphopanteth_bd.
CC InterPro; IPR006162; Pantane_S.
CC Pfam; PF00550; PP-binding; 1.
CC ProDom; PD000887; Acyl_carrier; 1.
CC TIGRfam; TIGR00517; acyl_carrier; 1.
CC PROSITE; PSS0075; ACP_DOMAIN; 1.
CC PROSITE; PSS0012; PHOSPHOPANTHEINE; FALSE_NEG.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
KW BINDING 37 37 phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8732 MW; E7BF70B5F7D4C77 CRC64;
Query Match 68.3%; Score 271; DB 1; Length 77;
Best Local Similarity 72.0%; Pred. No. 1.4e-15;
Matches 54; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
QY 6 ADTLERVTKIIVDRLCVDEADVKLEASFKEDELGADSLDYVELVMELEDFDEISDEDAE 65
DB 2 AEVFDRLVKEIILIDRLVLESKVTMEASFDDLDADSLDYVELVMELEDFDEISDEDAE 61
QY 66 KIATVGDAVNYIQNQ 80
DB 62 KINTVGDAVDYINSK 76

```

Search completed: December 21, 2005, 13:54:38
Job time : 119.075 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:44 ; Search time 10.4776 Seconds
(without alignments)
743.830 Million cell updates/sec

Title: US-10-717-138-1

Sequence: 397
1 GPLSGADTLERVTIKIIVDR.....EDAEKIAIVGDAVNTIQNOQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	93.2	77	2	JC4822 acyl carrier prote
2	313	78.8	77	2	B81361 acyl carrier prote
3	284	71.5	77	2	AF1300 acyl carrier prote
4	284	71.5	77	2	AF1672 acyl carrier prote
5	254	64.0	76	2	C64051 acyl carrier prote
6	244	61.5	77	2	T12052 acyl carrier prote
7	239	60.2	110	2	E82128 acyl carrier prote
8	236	59.4	77	2	F97115 acyl carrier prote
9	234	58.9	77	2	C89896 HmbB protein [impo
10	226.5	57.1	78	2	AC0195 acyl carrier prote
11	222	55.9	78	2	A70448 acyl carrier prote
12	220	55.4	78	2	T44435 acyl carrier prote
13	217.5	54.8	84	2	AG2223 acyl carrier prote
14	216	54.4	78	2	F81222 acyl carrier prote
15	215	54.2	78	1	AYEC acyl carrier prote
16	215	54.2	78	1	AE0642 acyl carrier prote
17	215	54.2	78	2	D85672 acyl carrier prote
18	215	54.2	78	2	H90812 acyl carrier prote
19	213	53.7	78	2	A83276 acyl carrier prote
20	212	53.4	78	2	T12021 acyl carrier prote
21	212	53.4	78	2	A36728 acyl carrier prote
22	211	53.1	77	2	H71541 probable acyl carr
23	209	52.6	78	2	AG2711 acyl carrier prote
24	209	52.6	78	2	AE3436 acyl carrier prote
25	204	51.4	78	2	C87457 acyl carrier prote
26	203	51.1	77	2	D81695 acyl carrier prote
27	202	50.9	110	2	S77465 acyl carrier prote
28	202	50.9	110	2	F75333 acyl carrier prote
29	201	50.6	78	2	H71922 acyl carrier prote

30	200.5	50.5	79	2	D83411 probable acyl carr
31	200	50.4	77	2	AC1388 acyl carrier prote
32	200	50.4	80	2	H84970 acyl carrier prote
33	197	49.6	79	2	G86527 acyl carrier prote
34	197	49.6	79	2	C72096 acyl carrier prote
35	196	49.4	81	2	C72349 acyl carrier prote
36	194	48.9	78	2	G64589 acyl carrier prote
37	193	48.6	80	2	S78295 acyl carrier prote
38	192.5	48.5	76	2	S13819 acyl carrier prote
39	192	48.4	80	2	A39452 acyl carrier prote
40	189	47.6	123	2	C71616 ACP Xf0672 [impor
41	188	47.4	85	2	G82776 acyl carrier prote
42	187	47.1	84	2	S73201 acyl carrier prote
43	184.5	46.5	153	2	B64640 acyl carrier prote
44	184	46.3	69	2	B6728 acyl carrier prote
45	176	44.3	80	2	C41609 acyl carrier prote

ALIGNMENTS

RESULT 1
JC4822
acyl carrier protein - Bacillus subtilis
N:Alternate names: 8.5K protein
C:Species: Bacillus subtilis
C:Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4822; A69582
R:Oguro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
A:Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, on
A:Reference number: JC4819; MUID:96257247; PMID:8654983
A:Accession: JC4822
A:Molecule type: DNA
A:Residues: 1-77 <OGU>
A:Cross-references: UNIPROT:P80643; UNIPARC:UP100000603BF; DDBJ:D64116; NID:G1389548; PI
R:Kunt, F.; Ogasawara, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho
A.; Enllich, S.D.; Emerson, P.T.; Emtan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, A.; Liu, H.; Maeda, S.; Maueel
A:Authors: Jauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maueel
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Setor
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69582
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-77 <KON>
A:Cross-references: UNIPARC:UP100000603BF; GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CT
A:Experimental source: strain 168
C:Genetics:
C:Gene: acpA; srb
C:Function:
A:Description: carrier of the growing fatty acid chain; growing fatty acid chain is cov
A:Pathway: fatty acid biosynthesis
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotei
F:2-73/Domain: acyl carrier protein homology <ACP>
F:37/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 93.2%; Score 370; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. NO. 4e-26;
Matches 76; Conservative 0; Indels 0; Gaps 0;

QY 6 ADTLERVTIKIIVDRIGVDEADVLTLSFKEDIGADSLDVVELVMELEDFMEISDEDBA 65

DB 2 ADLTERVTKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDEDAE 61
 QY 66 KIATVGDAVNYIQNOQ 81
 DB 62 KIATVGDAVNYIQNOQ 77

RESULT 2

B83961
 acyl carrier protein acpA [imported] - *Bacillus halodurans* (strain C-125)
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: B83961
 R:Takami, H.; Nakaone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: AB3650; PMID:20512582; PMID:11058132
 A:Accession: B83961
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <STO>
 A:Cross-references: UNIPROT:Q9KA04; UNIPARC:UPI0000125360; GB:AP001515; GB:BA000004; NID
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: acpA
 C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
 C:Keywords: carrier protein

Query Match 78.8%; Score 313; DB 2; Length 77;
 Best Local Similarity 81.6%; Pred. No. 4,2e-21;
 Matches 62; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 6 ADLTERVTKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDEDAE 65
 DB 2 ADLTERITKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDEDAE 61
 QY 66 KIATVGDAVNYIQNOQ 81
 DB 62 KIATVGDAVNYIQNOQ 77

RESULT 3

AF1300
 acyl carrier proteins homolog acpA [imported] - *Listeria monocytogenes* (strain EGD-e)
 C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AF1300
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A>Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; PMID:21537279; PMID:11679669
 A:Accession: AF1300
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <GLA>
 A:Cross-references: UNIPROT:Q92AK2; UNIPARC:UPI00000555AC; GB:NC_003210; PIDN:CAC9884.1
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: acpA
 C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
 C:Keywords: carrier protein

Query Match 71.5%; Score 284; DB 2; Length 77;
 Best Local Similarity 80.8%; Pred. No. 1.5e-18;
 Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 6 ADLTERVTKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDEDAE 65
 DB 62 KIATVGDAVNYIQNOQ 77

DB 2 AEVLEKVTKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDGDAB 61
 QY 66 KIATVGDAVNYIQ 78
 DB 62 NINTVGDAVKYIE 74

RESULT 4

AF1672
 acyl carrier protein homolog acpA [imported] - *Listeria innocua* (strain Ctip11262)
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AF1672
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A>Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; PMID:21537279; PMID:11679669
 A:Accession: AF1672
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <GLA>
 A:Cross-references: UNIPROT:Q92AK2; UNIPARC:UPI00000555AC; GB:AL592022; PIDN:CAC97150.1;
 A:Experimental source: strain Ctip11262
 C:Genetics:
 A:Gene: acpA
 C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
 C:Keywords: carrier protein

Query Match 71.5%; Score 284; DB 2; Length 77;
 Best Local Similarity 80.8%; Pred. No. 1.5e-18;
 Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 6 ADLTERVTKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDGDAB 65
 DB 2 AEVLEKVTKIIVDRLGVEADVKLEASFKEDELGADSLDVVELVMELEDFEFMEISDGDAB 61
 QY 66 KIATVGDAVNYIQ 78
 DB 62 NINTVGDAVKYIE 74

RESULT 5

C64051
 acyl carrier protein - *Haemophilus influenzae* (strain Rd KW20)
 C:Species: *Haemophilus influenzae*
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C:Accession: C64051
 R:Flitschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J
 A>Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A:Reference number: A64000; PMID:95350630; PMID:7542800
 A:Accession: C64051
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-76 <TIG>
 A:Cross-references: UNIPROT:P43709; UNIPARC:UPI0000125370; GB:U32701; GB:LA42023; NID:932
 C:Genetics:
 A:Gene: acpP
 C:Function:
 A:Description: carrier of the growing fatty acid chain; growing fatty acid chain is cova
 A:Pathway: fatty acid biosynthesis
 C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
 C:Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotein
 F1-72/Domain: acyl carrier protein homology <ACP>
 F36/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

C:Genetics:
A:Gene: asr3342
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein

Query Match 54.8%; Score 217.5; DB 2; Length 84;
Best Local Similarity 58.2%; Pred. No. 1.2e-12;
Matches 46; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 3 LGSADTLERVTIIVDRIGVDEAD-VKLEASFKEKDGADSLDVVELVWELDEPFMEISD 61
DB 1 MQSEFFKVKIVIEQLSVENPDVTPASRANLQADSLDVVELVWELDEPFMEISD 60

QY 62 EDAAKATVGAADVNIQO 80
DB 61 EAAEKITVQEAADVNIQO 79

RESULT 14

F81222
acyl carrier protein NMB0220 [imported] - Neisseria meningitidis (strain MCS8 serogroup

C:Species: Neisseria meningitidis

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: F81222; E81995
R:Retellein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.
Science 287, 1809-1815, 2000

A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.

A:Reference number: A81000; MUID:2015755; PMID:10710307

A:Accession: F81222

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-78 <RPT>

A:Cross-references: UNIPROT:Q9UR72; UNIPARC:UPI0000125376; GB:AE002380; GB:AE002098; NID

A:Experimental source: serogroup B, strain MCS8

R:Parhill, J.; Achman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: E81995

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-78 <PAR>

A:Cross-references: UNIPARC:UPI0000125376; GB:AL157959; NID:97378778; PIDN:

A:Experimental source: serogroup A, strain Z2491

C:Keywords: carrier protein

C:Keywords: acyl carrier protein homology

F:2-73/Domain: acyl carrier protein homology <ACP>

Query Match 54.4%; Score 216; DB 2; Length 78;
Best Local Similarity 64.7%; Pred. No. 1.5e-12;
Matches 44; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 10 ERYTKIIVDLGVDEADVTLKASFKEDLGADSLDVVELVWELDEPFMEISDDEAKIAT 69
DB 6 QQVKKIIVAEQLGVDEADVKNESFODDLGADSLDVVELVWELDEPFMEISDDEAKIAT 65

QY 70 VGDVAVNYI 77
DB 66 VQALADYI 73

RESULT 15

AYEC
acyl carrier protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 24-Apr-1984 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C:Accession: C42147; A92042; A26935; C64853; S28389; A03358

R:Rawlings, M.; Cronan Jr., J.E.

J. Biol. Chem. 267, 5751-5754, 1992

A:Title: The gene encoding Escherichia coli acyl carrier protein lies within a cluster o

A:Reference number: A42147; MUID:92210530; PMID:1556094

A:Accession: C42147

A:Molecule type: DNA

A:Residues: 1-78 <RAW>

A:Cross-references: UNIPROT:P02901; UNIPARC:UPI0000059F9B; GB:M84991; NID:G145879; PIDN:

A:Experimental source: strain E-26

R:Vanaman, T.C.; Wakil, S.J.; Hill, R.L.

J. Biol. Chem. 243, 6420-6431, 1968

A:Title: The complete amino acid sequence of the acyl carrier protein of Escherichia col

A:Reference number: A92042; MUID:69063911; PMID:4882207

A:Accession: A92042

A:Molecule type: protein

A:Residues: 2-24, 'D', '26-78 <VAN>

A:Cross-references: UNIPARC:UPI000017469E

R:Vanaman, T.C.; Wakil, S.J.; Hill, R.L.

J. Biol. Chem. 243, 6409-6419, 1968

A:Title: The preparation of tryptic, peptic, thermolysin, and cyanogen bromide peptides

A:Reference number: A92041; MUID:69063910; PMID:4882206

A:Contents: annotation; partial sequence

R:Jackowski, S.; Rock, C.O.

J. Bacteriol. 169, 1469-1473, 1987

A:Title: Altered molecular form of acyl carrier protein associated with beta-ketoacyl-ac

A:Reference number: A26935; MUID:87165751; PMID:3549687

A:Accession: A26935

A:Molecule type: protein

A:Residues: 2-43, 'I', '45-78 <JAC>

A:Cross-references: UNIPARC:UPI000017469F

A:Experimental source: strain K-12

R:Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64853

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-78 <BLAT>

A:Cross-references: UNIPARC:UPI0000059F9B; GB:AE000210; GB:U00096; NID:G1787332; PIDN:AA

A:Experimental source: strain K-12, substrain MG1655

R:Niki, H.; Imanura, R.; Kitoaka, M.; Yamanaka, K.; Ogura, T.; Hiraga, S.

EMBO J. 11, 5101-5109, 1992

A:Title: E. coli MubB protein involved in chromosome partition forms a homodimer with a

A:Reference number: S28389; MUID:93099885; PMID:1464330

A:Accession: S28389

A:Molecule type: protein

A:Residues: 2-25, 'X', '27-35, 'XX', '38-41 <NIK>

A:Cross-references: UNIPARC:UPI00001746A0

C:Genetics:

A:Gene: acpP

C:Function:

A:Description: carrier of the growing fatty acid chain; growing fatty acid chain is cov

C:Keywords: acyl/peptidyl carrier protein; acyl carrier protein homology

C:Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotei

F:2-73/Domain: acyl carrier protein homology <ACP>

F:37/Binding site: phosphopantetheine (Ser) (covalent) #status experimental

Query Match 54.2%; Score 215; DB 1; Length 78;
Best Local Similarity 63.9%; Pred. No. 1.9e-12;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIVDLGVDEADVTLKASFKEDLGADSLDVVELVWELDEPFMEISDDEAKIAT 69
DB 6 ERYKKIIVGQLGVKQSEVNNMSFVEDLGADSLDVVELVWELDEPFMEISDDEAKIAT 65

QY 70 VGDVAVNYIQOQ 81
DB 66 VQALADYINGHQ 77

Thu Dec 22 11:00:01 2005

us-10-717-138-1.rpr

Page 6

Search completed: December 21, 2005, 13:49:38
Job time : 10.4776 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:03 ; Search time 107.194 Seconds
(without alignments)
332.012 Million cell updates/sec

Title: US-10-717-138-1

Sequence: 1 GPLGSADTLERVTKIIVRL.....EDAKIATVGDAVNTIQNOQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseq21980s:*
2: geneseq21990s:*
3: geneseq22000s:*
4: geneseq22001s:*
5: geneseq22002s:*
6: geneseq22003as:*
7: geneseq22003bs:*
8: geneseq22004s:*
9: geneseq22005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	81	5	AAU10693 B. subtil
2	307	77.3	80	5	ABU18284 Protein e
3	284	71.5	77	5	ABBA49632 Listeria
4	284	71.5	77	6	ABU32958 Protein e
5	254	64.0	76	4	AAU35380 Haemophil
6	254	64.0	76	6	ABU30165 Protein e
7	249	62.7	76	6	ABU39519 Protein e
8	239	60.2	110	6	ABU49449 Protein e
9	238	59.9	77	6	ABU43867 Protein e
10	238	59.9	77	6	ABU42995 Protein e
11	238	59.9	79	5	ABP39964 Staphyloc
12	238	59.9	79	8	ADSO6306 Staphyloc
13	236	59.4	77	6	ABU23599 Protein e
14	234	58.9	77	4	AAU37508 Staphyloc
15	234	58.9	77	4	AAU37209 Staphyloc
16	234	58.9	77	4	AAU37209 Staphyloc
17	234	58.9	77	4	AAU37209 Staphyloc
18	234	58.9	77	6	ABM73195 Staphyloc
19	234	58.9	77	9	ADW94686 Proteolitea
20	232	58.4	73	4	AAU33966 Staphyloc
21	227	58.4	77	4	AAU36531 Staphyloc
22	227	57.2	79	6	ABU23521 Protein e
23	226	57.1	78	6	ABU50649 Protein e
24	225	56.7	94	7	ADF07671 Bacterial

25	225	56.7	104	6	ABU24629 Protein e
26	223.5	56.3	48	5	AAU47181 Modular e
27	223.5	56.3	75	8	ADN25869 Bacterial
28	222.5	56.0	72	8	ADN24411 Bacterial
29	222.5	56.0	78	8	ADN21655 Bacterial
30	222.5	56.0	79	6	ABU19977 Protein e
31	222.5	56.0	79	6	ABU22402 Protein e
32	222.5	56.0	79	6	ABU21577 Protein e
33	222.5	56.0	80	9	ABM95361 M. xanthu
34	222	55.9	78	8	ADN17479 Bacterial
35	222	55.9	80	6	ADN10328 Allotococ
36	220	55.4	75	8	ADN24605 Bacterial
37	220	55.4	82	6	ABU33189 Protein e
38	220	55.4	82	9	ABE31501 L. pneumo
39	220	55.4	98	9	ABE38214 L. pneumo
40	217	54.7	71	8	ADN26458 Bacterial
41	217	54.7	76	8	ADN21595 Bacterial
42	217	54.7	78	6	ABP80257 N. gonorr
43	217	54.7	78	6	ABP78733 N. gonorr
44	217	54.7	78	6	ABU37226 Protein e
45	217	54.7	90	6	ABP78743 N. gonorr

ALIGNMENTS

RESULT 1
AAU10693
AAU10693 standard; protein; 81 AA.
XX
AC AAU10693;
DT 25-FEB-2002 (first entry)
DE
XX B. subtilis ACP used to grow ACP/ACPS complex crystals.
XX
XX Crystal structure; acyl carrier protein synthase; acyl carrier protein;
KM rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-pant;
KW ACP/ACPS complex; protein co-ordinate data.
XX
XX Bacillus subtilis.
XX
XX MO200185743-A2.
XX
PD 15-NOV-2001.
XX
PF 26-JAN-2001; 2001WO-US002949.
XX
PR 08-MAY-2000; 2000US-0202466P.
XX
XX (AMHP) AMERICAN HOME PROD CORP.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Paritis KD, Somers WS, Tam AS, Lin LL, Stahl ML, Powers R, Xu G;
DR WPI; 2002-055580/07.
XX
XX Crystallized complex useful in rational drug design methods, comprises
PT acyl carrier protein synthase and acyl carrier protein.
XX
XX Example 1; Fig 1; 147pp; English.
PS
XX The present invention relates to a crystallised structure comprising acyl
XX carrier protein synthase (ACPS) complexed with acyl carrier protein
XX (ACP). The invention also describes the solution structure of Bacillus
XX subtilis ACP. Both these structures are useful in rational drug design
XX methods for identifying agents that may interact with active sites of
XX ACPs and ACP, and for testing these agents to identify agents that may
XX represent novel antibiotics. They are also useful for design and
XX selection of potent and selective agents which interact with ACPs and
XX ACP, and for the design of antibiotics and other agents that interfere
XX with 4'-phosphopantetheinyl (P-pant) attachment, thus preventing
XX activation of corresponding carrier proteins. The present sequence

CC represents B. subtilis ACP used to grow ACP/ACPS complex crystals
XX SQ Sequence 81 AA;
Query Match 100.0%; Score 397; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFLGSADTLERVTIKIYDRLGVDEADVKLKASFKEDLGADSLDVVELVMELEDFEIMSD 60
DB 1 GFLGSADTLERVTIKIYDRLGVDEADVKLKASFKEDLGADSLDVVELVMELEDFEIMSD 60
QY 61 DEDAEKATVGDVAVNYIQNQ 81
DB 61 DEDAEKATVGDVAVNYIQNQ 81
RESULT 2
ABU18284
ID ABU18284 standard; protein; 80 AA.
XX AC ABU18284;
XX DT 19-JUN-2003 (first entry)
XX OS Protein encoded by Prokaryotic essential gene #3811.
XX KW Antisense, prokaryotic essential gene; cell proliferation; drug design.
XX OS Bacillus anthracis.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JM;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX N-PSDB; ACA22154.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 46208; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway of
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 80 AA;
Query Match 77.3%; Score 307; DB 6; Length 80;
Best Local Similarity 82.9%; Pred. No. 1.9e-26;
Matches 63; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 4 GSADTLERVTIKIYDRLGVDEADVKLKASFKEDLGADSLDVVELVMELEDFEIMSD 63
DB 3 GMADVLERVTIKIYDRLGVDEETVVPASFKEDLGADSLDVVELVMELEDFEIMSD 62
QY 64 AEKATVGDVAVNYION 79
DB 63 AEKATVGDVAVNYIES 78
RESULT 3
ABB49632
ID ABB49632 standard; protein; 77 AA.
XX AC ABB49632;
XX DT 05-FEB-2002 (first entry)
XX OS Listeria monocytogenes protein #2336.
XX DE Listeria monocytogenes protein #2336.
XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX KW vitamin B12; bacterial infection; disease.
XX OS Listeria monocytogenes.
XX PN WO200177335-A2.
XX PD 18-OCT-2001.
XX PF 11-APR-2001; 2001WO-FR001118.
XX PR 11-APR-2000; 2000FR-00004629.
XX PA (INSP) INST PASTEUR.
XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
XX PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
XX PI Daniels J, Goebel W, Kretz U, Kuhn M, Ng B, Vazquez-Boland JA;
XX PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
XX PI Charrabory T, Doman E, Hain T, Berche P, Charbit A, Durant L;
XX PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
XX PI Madueno E, De Pablos B, Wehlend U, Kaerst U, Entian K, Hauf J;
XX PI Rose M, Voss H;
XX DR WPI; 2002-010914/01.
XX CC Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX CC and prevention of Listeria and related bacterial infections, and related
XX CC polypeptides.
XX PS Claim 6; SEQ ID NO 2337; 192pp; French.

CC The present invention relates to the genome sequence of *Listeria*
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in *L.*
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of *L. monocytogenes* and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccines compositions for the treatment or prevention of infections by *L.*
 CC monocytogenes and related organisms. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 77 AA;

Query Match 71.5%; Score 284; DB 5; Length 77;
 Best Local Similarity 80.8%; Pred. No. 6, 6e-24;
 Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTLERVTKIIVDRIGVDEADVLTLSFKEDIGADSLDVVELVMELEDFMEISDEDAE 65
 :||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
 Db 2 AEVLEKVTKIIVDRIGVDEADVLTLSFKEDIGADSLDVVELVMELEDFMEISDGDAB 61

OY 66 KIATVGDVANYIQ 78
 :|||||||:
 Db 62 NINTVGDVAVXYIE 74

RESULT 4
 ABU32958
 ID ABU32958 standard; protein; 77 AA.

XX ABU32958;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #18485.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS *Listeria monocytogenes*.

XX MO200277183-A2.

XX 03-OCT-2002.

PF 21-MAR-2002; 2002MO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362659P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GF, Yamamoto R, Foreyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA36828.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 60882; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 77 AA;

Query Match 71.5%; Score 284; DB 6; Length 77;
 Best Local Similarity 80.8%; Pred. No. 6, 6e-24;
 Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTLERVTKIIVDRIGVDEADVLTLSFKEDIGADSLDVVELVMELEDFMEISDEDAE 65
 :||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
 Db 2 AEVLEKVTKIIVDRIGVDEADVLTLSFKEDIGADSLDVVELVMELEDFMEISDGDAB 61

OY 66 KIATVGDVANYIQ 78
 :|||||||:
 Db 62 NINTVGDVAVXYIE 74

RESULT 5
 AAU35380
 ID AAU35380 standard; protein; 76 AA.

XX AAU35380;

DT 14-FEB-2002 (first entry)

DE Haemophilus influenzae cellular proliferation protein #21.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.

XX Haemophilus influenzae.

XX MO200170955-A2.

XX 27-SEP-2001.

PF 21-MAR-2001; 2001MO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR	25-OCT-2001; 2001US-0342923P.	
PR	08-FEB-2002; 2002US-00072851.	
PR	06-MAR-2002; 2002US-0362659P.	
XX		
XX	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;	
PI	Wall D, Trivick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;	
XX		
DR	WPI: 2003-029926/02.	
XX		
XX	N-PSDB; ACA34035.	
PT	New antisense nucleic acids, useful for identifying proteins or screening	
PT	for homologous nucleic acids required for cellular proliferation to	
PT	isolate candidate molecules for rational drug discovery programs.	
XX		
PS	Claim 25; SEQ ID NO 58089; 1766pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid comprising any one of	
CC	the 6213 antisense sequences given in the specification where expression	
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:	
CC	(1) a vector comprising a promoter operably linked to the nucleic acid	
CC	encoding a polypeptide whose expression is inhibited by the antisense	
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated	
CC	polypeptide or its fragment whose expression is inhibited by the	
CC	antisense nucleic acid; (4) an antibody capable of specifically binding	
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	
CC	proliferation or the activity of a gene in an operon required for	
CC	proliferation; (7) identifying a compound that influences the activity of	
CC	the gene product or that has an activity against a biological pathway	
CC	required for proliferation, or that inhibits cellular proliferation; (8)	
CC	identifying a gene required for cellular proliferation or the biological	
CC	pathway in which a proliferation-required gene or its gene product lies	
CC	or a gene on which the test compound that inhibits proliferation of an	
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a	
CC	compound's activity; (11) a culture comprising strains in which the gene	
CC	product is overexpressed or underexpressed; (12) determining the extent	
CC	to which each of the strains is present in a culture or collection of	
CC	strains; or (13) identifying the target of a compound that inhibits the	
CC	proliferation of an organism. The antisense nucleic acids are useful for	
CC	identifying proteins or screening for homologous nucleic acids required	
CC	for cellular proliferation to isolate candidate molecules for rational	
CC	drug discovery programs, or for screening homologous nucleic acids	
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,	
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of	
CC	the target prokaryotic essential genes. Note: The sequence data for this	
CC	patent did not form part of the printed specification, but was obtained	
CC	in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
XX		
SO	Sequence 76 AA;	
QY	Query Match 64.0%; Score 254; DB 6; Length 76;	
QY	Best Local Similarity 72.2%; Pred. No. 1,4e-20;	
QY	Matches 52; Conservative % 8; Mismatches 12; Indels 0; Gaps 0;	
QY	10 ERYVRIIVDRIGVDEAVYKLEAFKFDLGADSLVVELVWELDEDFPMDEISDDEAKIAT 69	
QY	: : : : : : : : : :	
QY	5 ERYVKITVEQLGVVEEDVKPEASFVEDLGDASLDVTELVAALBEEFDLEIPDEBAKITTT 64	
QY	70 VGDAVNYIONQO 81	
QY	: : : : : : : : :	
QY	65 VQSAIDVYQNNQ 76	
Db		
RESULT 7		
ID	ABU39519 standard; protein; 76 AA.	
XX	ABU39519;	
AC		
XX		
DT	19-JUN-2003 (first entry)	

CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 110 AA;

Query Match 60.2%; Score 239; DB 6; Length 110;
Best Local Similarity 72.1%; Pred. No. 1,1e-18; Indels 0; Gaps 0;
Matches 49; Conservative 9; Mismatches 10;

QY 10 ERVTKIIVDRIGVDEADVLEASFKEDLGADSLDVLELWMELEDFDMEISDEDAEKIAT 69
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 38 ERVKKIIVBQGVDEAEVAVNESSFVBDLGADSLDVLELWMALEEDDTETIPDEAEKITT 97
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 70 VGDVAVNYI 77
|:::|
DB 98 VQAAIDYV 105

RESULT 9

ABU43867 standard; protein; 77 AA.

ABU43867;

19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #29394.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Staphylococcus haemolyticus.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI, 2003-029926/02.

New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 71791; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 77 AA;

Query Match 59.9%; Score 238; DB 6; Length 77;
Best Local Similarity 67.1%; Pred. No. 8.8e-19; Indels 0; Gaps 0;
Matches 49; Conservative 8; Mismatches 16;

QY 7 DTLERVTKIIVDRIGVDEADVLEASFKEDLGADSLDVLELWMELEDFDMEISDEDAEK 66
|:::|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 2 ENFDKVIIDVDRIGVDAKXTEDASFKDDLGADSLDVLELWMELEDFDMEISDEDAEK 61
|:::|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 67 IATVGDVAVNYIQN 79
|:::|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 62 INTVGDVAVKYN 74

RESULT 10

ABU42995 standard; protein; 77 AA.

ABU42995;

19-JUN-2003 (first entry)

Protein encoded by Prokaryotic essential gene #28522.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Staphylococcus epidermidis.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI, 2003-029926/02.

New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 70919; 1766pp; English.

PT treating an *S. epidermidis* bacterial infection.
XX
PS Claim 17; SEQ ID NO 5601; 741pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a nucleotide
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
CC 1-3772) and encoding an *Staphylococcus epidermidis* polypeptide with any
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
CC given in the specification. Also described are: a recombinant expression
CC vector; a cell comprising a recombinant expression vector of (1);
CC producing an *S. epidermidis* polypeptide; an isolated nucleic acid
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
CC vaccine composition for prevention or treatment of an *S. epidermidis*
CC infection, comprising a nucleic acid cited above and a carrier; treating
CC a subject for *S. epidermidis* infection; a recombinant or substantially
CC pure preparation of an *S. epidermidis* polypeptide or its fragment; a
CC vaccine composition for prevention or treatment of an *S. epidermidis*
CC infection; detecting the presence of a *Staphylococcus* nucleic acid in a
CC sample; a computer readable medium having recorded in it the nucleotide
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
CC system for identifying fragments of the *Staphylococcus* genome of
CC commercial importance; a computer based system for identifying fragments
CC of the *Staphylococcus* plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the *Staphylococcus*
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the *Staphylococcus* genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an *Staphylococcus epidermidis* bacterial
CC infection. This is the amino acid sequence of a *S. epidermis* protein of
CC the invention.
SQ Sequence 79 AA:
SQ
Query Match 59.9%; Score 238; DB 8; Length 79;
Best Local Similarity 67.1%; Pred. No. 9.1e-19;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 7 DTLERVTKIIVRLGADVADVLKASFKEDLGAISLVLVWLEDEDFDMEISPDAAK 66
DB 4 ENFDKXKDIIVRLGADVADVLKASFKEDLGAISLVLVWLEDEDFDMEISPDAAK 63
QY 67 IATVGDVAVNYION 79
DB 64 INTVGDVAVKXINS 76
Db
RESULT 13
ABU23599
ID ABU23599 standard; protein; 77 AA.
XX
AC ABU23599;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #9126.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS *Clostridium acetobutylicum*.
XX
PN WO20027183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
XX
PR 25-OCT-2001; 2001US-0342823P.
XX
PR 08-FEB-2002; 2002US-00072851.
XX
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX
DR N-PSDB; ACA27469.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
PS Claim 25; SEQ ID NO 51523; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway
CC of the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 77 AA:
SQ
Query Match 59.4%; Score 236; DB 6; Length 77;
Best Local Similarity 60.9%; Pred. No. 1.5e-18;
Matches 42; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
QY 10 ERYVKIIVRLGADVADVLKASFKEDLGAISLVLVWLEDEDFDMEISPDAAKAT 69
DB 4 EKVXDIADQIGIDATETKXSSFTDDLGASDVLVWLEDEDFDMEISPDAAKXVS 63
QY 70 VGDVAVNYIQ 78
DB 64 VGDVAVNYIK 72
Db
RESULT 14
AAU37508
ID AAU37508 standard; protein; 77 AA.
XX
AC AAU37508;
XX
DT 14-FEB-2002 (first entry)
XX
DE *Staphylococcus aureus* cellular proliferation protein #1678.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX

OS		Staphylococcus aureus.
XX		
PN		W0200170955-A2.
XX		
PD		27-SEP-2001.
XX		
PF		21-MAR-2001; 2001WO-US009180.
XX		
PR	21-MAR-2000;	2000US-0191078P.
PR	23-MAY-2000;	2000US-0206848P.
PR	26-MAY-2000;	2000US-0207727P.
PR	23-OCT-2000;	2000US-0242578P.
PR	27-NOV-2000;	2000US-0253625P.
PR	22-DEC-2000;	2000US-0257931P.
PR	16-FEB-2001;	2001US-0269308P.
PA	(ELIT-)	ELITRA PHARM INC.
XX		
P1	Haselbeck R,	Ohlson KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
P1	Yamamoto RT,	Xu HH;
XX		
DR	MP1; 2001-611495/70.	
DR	N-PsDB; AAS55367.	
XX		
PT	New polynucleotides for the identification and development of	
PT	antibiotics, comprise sequences of antisense nucleic acids.	
PS	Example 3; SEQ ID NO 13101; 511pp; English.	
XX		
CC	The invention relates to antisense inhibitors of genes essential to	
CC	prokaryotic cellular proliferation, their use in identifying the genes,	
CC	their use in the discovery of novel antibiotics, the essential genes	
CC	themselves and the encoded proteins. The prokaryotes used are Escherichia	
CC	coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,	
CC	Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also	
CC	useful for the identification of potential new targets for antibiotic	
CC	development. The antisense nucleic acids can also be used to identify	
CC	proteins used in proliferation, to express these proteins, and to obtain	
CC	antibodies capable of binding to the expressed proteins. The proteins can	
CC	be used to screen compounds in rational drug discovery programmes. The	
CC	antisense nucleic acid sequence is also useful to screen for homologous	
CC	nucleic acids which are required for cell proliferation in a wide variety	
CC	of organisms. The present sequence represents an essential prokaryotic	
CC	cellular proliferation protein. Note: The sequence data for this patent	
CC	did not form part of the printed specification, but was obtained in	
CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 77 AA;	
	Query Match	58.9%; Score 234; DB 4; Length 77;
	Best Local Similarity	65.8%; Pred No.2.5e-18;
	Matches	48; Conservative
Oy	7 DTLERVTIKIIVRLGADVDYKLEASFREDLGGADSLDVVELVMELEDFDMEISDEDAEK 66	
Dd	2 ENPDFDKOIIIVRLRGVDADKVTEADSPFDKDDLGADSLDIALIELVMELEDFEFGIEIPDEAEAK 61	
Oy	67 IATVGDAVVYION 79	
Dd	62 INTVGDAVKEFINS 74	
RESULT 15		
ID	AAU37209	
XX	AAU37209 standard; protein; 77 AA.	
AC	AAU37209;	
XX		
DT	14-FEB-2002 (first entry)	
XX		
DE	Staphylococcus aureus cellular proliferation protein #1379.	

```

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX OS Staphylococcus aureus.
XX EN WO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX FR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Ohlsen KU, Zyekind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
DR WPI; 2001-611495/70.
DR N-PSTB; AAS55068.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 12802; 51bp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 77 AA;
SQ
Query Match 58.9%; Score 234; DB 4; Length 77;
Best Local Similarity 65.8%; Pred. No. 2.5e-18;
Matches 48; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
QY 7 DTLEKVTIIVDRIGVDADVRLKLSAFKEDSGADSLDVELVMLEDFDEMEISDEDPAEK 66
DB 2 ENFDPEKVIIVDRIGVDADVRLKTSFDDIDGADSLDLALVMLEDFDFGEIDBEBAEK 61
QY 67 IATVGDAVNYYTQN 79
DB 62 INTVGDAVKFINLS 74

```

This Page Blank (uspto)